

SEARCH REQUEST FORM**Scientific and Technical Information Center**

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: <u>D. Schreder</u>	NA Sequence (#) _____	STN _____
Searcher Phone #: <u>308-4292</u>	AA Sequence (#) <u>16</u>	Dialog _____
Searcher Location: <u>CM 16403</u>	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: _____	Bibliographic _____	Dr.Link _____
Date Completed: <u>4/1</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: <u>37</u>	Fulltext _____	Sequence Systems <u>CompuLink JLG</u>
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: <u>39</u>	Other _____	Other (specify) _____

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 15:09:54 ; Search time 85.18 Seconds
(without alignments)
206.967 Million cell updates/sec

Title: US-09-499-662-109

Perfect score: 1245

Sequence: 1 METDTILLWLLVPGSTG.....EVTHQGLSSPVTKSFNRGEC 238

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_1101.*
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18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1245	100.0	238	19 AAW83035	Anti-Fas humanised
2	1245	100.0	238	21 AAB14778	Humanised anti-Fas
3	1245	100.0	238	21 AAW90928	Humanised HFE7A de
4	1239	99.5	238	19 AAW83032	Anti-Fas humanised
5	1239	99.5	238	21 AAB14773	Humanised anti-Fas
6	1239	99.5	238	21 AAW90923	Humanised anti-Fas
7	1231	98.9	238	19 AAW83033	Anti-Fas humanised
8	1231	98.9	238	21 AAB14774	Humanised anti-Fas
9	1231	98.9	238	21 AAW90924	Humanised anti-Fas
10	1207	96.9	238	19 AAW83034	Anti-Fas humanised
11	1207	96.9	238	21 AAB14777	Humanised anti-Fas

12	1207	96.9	238	21 AAW90927	Humanised HFE7A de
13	1195	96.0	238	19 AAW83031	Anti-Fas humanised
14	1195	96.0	238	21 AAB14772	Humanised anti-Fas
15	1195	96.0	238	21 AAW90922	Humanised anti-Fas
16	1158	93.0	238	21 AAW90931	Humanised anti-Fas
17	1155	92.8	238	21 AAW90932	Humanised anti-Fas
18	1154	92.7	238	21 AAW90930	Humanised anti-Fas
19	1038.5	83.4	235	21 AAY93702	The kappa chain of
20	1038.5	83.4	235	21 AAY93729	The kappa chain of
21	1031	82.8	218	18 AAW13563	Humanised anti-L-s
22	1029	82.7	234	21 AAY92239	Human bone marrow-
23	1027	82.5	240	20 AAY50161	Human reshaped F19
24	1024	82.2	234	21 AAY93708	The kappa chain of
25	1024	82.2	234	21 AAY93733	The kappa chain of
26	1021.5	82.0	233	21 AAY93704	The kappa chain of
27	1021.5	82.0	233	21 AAY93731	The kappa chain of
28	1017	81.7	218	20 AAW95658	Mus musculus anti-
29	1017	81.7	218	21 AAY85200	Light chain amino
30	1017	81.7	218	22 AAB76947	Full variable ligh
31	1010	81.1	218	14 AAR33312	Humanised MaEl1 Ve
32	1006	80.8	236	22 AAG71272	Human gene 2-encod
33	1006	80.8	237	20 AAW73873	Human antiFc epsil
34	1003.5	80.6	384	22 AAU14461	Human novel protei
35	1003.5	80.6	384	22 AAU14462	Human novel protei
36	1003.5	80.6	384	22 AAU14464	Human novel protei
37	1003.5	80.6	384	22 AAU14464	Human novel protei
38	1000	80.3	240	20 AAW73875	Human antiFc epsil
39	994	79.8	218	20 AAV50030	Human E27 anti-IgE
40	994	79.8	218	20 AAW95660	Mus musculus anti-
41	994	79.8	218	20 AAW95662	Mus musculus anti-
42	994	79.8	218	21 AAB07472	Amino acid sequenc
43	994	79.8	218	22 AAB74211	E27 anti-IgE antib
44	991	79.6	218	20 AAW95669	Mus musculus anti-
45	991	79.6	218	20 AAW95664	Mus musculus anti-

ALIGNMENTS

RESULT	1
AAW83035	AAW83035 standard; Protein; 238 AA.
ID	AAW83035
AC	AAW83035;
XX	15-MAR-1999 (first entry)
DT	XX
DE	Anti-Fas humanised antibody:HFE7A light chain PDHM type.
KW	HFE7A; monoclonal antibody;mouse; Fas; humanised antibody;
KW	apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
KW	systemic lupus erythematosus; graft versus host disease;
KW	Sjogren syndrome; pernicious anaemia; Addison's disease;
KW	scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KW	rheumatoid arthritis; autoimmune haemolytic anaemia;
KW	myasthenia gravis; multiple sclerosis; Basedow's disease;
KW	thrombopenia purpura; insulin-dependent diabetes; allergy;
KW	atopy; arteriosclerosis; myocarditis; cardiomyopathy; AIDS;
KW	glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KW	transplant rejection; therapy.
XX	Homo sapiens.
OS	Synthetic.
XX	XX
FH	Key Location/Qualifiers
FT	Peptide 1..20
FT	/label= Sig_peptide 21..238
FT	Protein /label= Mat:protein 21..131
FT	Region /label= Variable 132..238
FT	Region /label= Constant

QY 1 METDTILLWVLLWVPGSTGEIVLTQSPGTLISLSPGERATLISCKASQSVVDGDSYMMNY 60
 Db 1 metdtillwvllwvpgstgeivltqspgtlslspperatlsckasqsvdydgsymny 60
 QY 61 QOKPQAPRLIIYAASNLSEGIPIRFGSGSGTDFTLTIHPVEEDAATYYCQSNEDPR 120
 Db 61 qkqpqaprllyiaasnlesgipdrfsgsgsgtdftltihpveedaatyycqsgnedpr 120
 QY 121 TFGQGTLEIKRTVAAPSVFIIPPSDEQLKSGTASVVCLLNPNFYPREAKVQWKVDNALQS 180
 Db 121 tfgggtkleikrtvaapsvfiiippsdeqlksgtasvvcvllnfnfpreakvqwkvdnalqs 180
 QY 181 GNSQESVTEQSDKSTYSLSTLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 Db 181 gnsqesvteqsdkstyslsstltlskadyekkhkyacevthqglsspvtksfnrgec 238

RESULT 3
 AAW90928
 ID AAW90928 standard; Protein; 238 AA.
 AC AAW90928;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Humanised HFE7A designed light chain protein #2.
 XX
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiatherosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX
 OS Synthetic.
 XX
 PN EP990663-A2.
 XX
 PD 05-APR-2000.
 XX
 PF 29-SEP-1999; 99EP-0307711.
 XX
 PR 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX
 DR WPI; 2000-258930/23.
 DR N-PSDB; AAA11615.
 XX
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems -
 XX
 PS Example reference 21; Page 144-145; 263pp; English.
 XX
 CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiatherosclerotic, cardiac and hepatotropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive

CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A designed light chain which is used in
 CC the method described in the invention.

XX Sequence 238 AA;
 SQ

Query Match 100.00% Score 1245; DB 21; Length 238;
 Best Local Similarity 100.00% Pred. No. 5.2e-67;
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METDTILLWVLLWVPGSTGEIVLTQSPGTLISLSPGERATLISCKASQSVVDGDSYMMNY 60
 Db 1 metdtillwvllwvpgstgeivltqspgtlslspperatlsckasqsvdydgsymny 60
 QY 61 QOKPQAPRLIIYAASNLSEGIPIRFGSGSGTDFTLTIHPVEEDAATYYCQSNEDPR 120
 Db 61 qkqpqaprllyiaasnlesgipdrfsgsgsgtdftltihpveedaatyycqsgnedpr 120
 QY 121 TFGQGTLEIKRTVAAPSVFIIPPSDEQLKSGTASVVCLLNPNFYPREAKVQWKVDNALQS 180
 Db 121 tfgggtkleikrtvaapsvfiiippsdeqlksgtasvvcvllnfnfpreakvqwkvdnalqs 180
 QY 181 GNSQESVTEQSDKSTYSLSTLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 Db 181 gnsqesvteqsdkstyslsstltlskadyekkhkyacevthqglsspvtksfnrgec 238

RESULT 4
 AAW83032
 ID AAW83032 standard; Protein; 238 AA.
 XX
 AC AAW83032;
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE Anti-Fas humanised antibody HFE7A light chain HM type.
 XX
 KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy.

OS Homo sapiens.
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Peptide 1..20
 FT Protein /label= Sig-peptide
 FT 21..238
 FT /label= Mat-protein
 FT Region 21..131

Best Local Similarity 99.2%; Pred. No. 1.2e-66; Matches 236; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 METDTILLWVLLWVPGSTGEIVLTQSPGTLSLSPGERATLSCSKASQSDYDGDSDYNNWY 60
 D 1 metdtillwvllwvpgstgdvltqspgtlsispgeratlsckasqsdvdygdsymwy 60

QY 61 QOKPQAPRLIYAASNLGSDIPRFGSGSGTDFTLTIHPVEEDAATYYCQSQSNEPDR 120
 D 61 qokpqaprllyaaasnlsgipdrfsgsgsgtdftltihpveedaatyycqsqnedpr 120

QY 121 TFGOGTKLEIKRTVAAPSVFIPPSDEQLKSGTASVCLLNFPRAKVKQVNDNALQS 180
 D 121 tfgogtkleikrtvaapsvfippsdeqlksgtasvcllnfpreakvkqvdnalqs 180

QY 181 GNSQESVTEQDSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 D 181 gnsqesvteqdsksstyslsltltlskadyekkhkvyacevthqglsspvtksfnrgec 238

RESULT 6
 AAW90923
 ID AAW90923 standard; Protein; 238 AA.
 AC AAW90923;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Humanised anti-Fas antibody HFE7A light chain HM type protein.
 XX
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
 KW dermatologic; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX
 OS Synthetic.
 XX
 XX EP990663-A2.
 XX
 PN 05-APR-2000.
 XX
 PD 29-SEP-1999; 99EP-0307711.
 XX
 PF 30-SEP-1998; 98JP-0276881.
 XX
 PR 30-SEP-1998; 98JP-0276882.
 XX
 XX (SANY) SANKYO CO LTD.
 PA
 PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX
 XX WPI: 2000-258930/23.
 DR
 DR N-PSDB; AAA11563.
 XX
 FT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems -
 XX
 XX Example reference 14; Page 117-118; 263pp; English.
 PS
 XX
 CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,

CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A light chain HM type which is used in
 CC the method described in the invention.
 XX
 SQ Sequence 238 AA;

Query Match 99.5%; Score 1239; DB 21; Length 238;
 Best Local Similarity 99.2%; Pred. No. 1.2e-66;
 Matches 236; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 METDTILLWVLLWVPGSTGEIVLTQSPGTLSLSPGERATLSCSKASQSDYDGDSDYNNWY 60
 D 1 metdtillwvllwvpgstgdvltqspgtlsispgeratlsckasqsdvdygdsymwy 60

QY 61 QOKPQAPRLIYAASNLGSDIPRFGSGSGTDFTLTIHPVEEDAATYYCQSQSNEPDR 120
 D 61 qokpqaprllyaaasnlsgipdrfsgsgsgtdftltihpveedaatyycqsqnedpr 120

QY 121 TFGOGTKLEIKRTVAAPSVFIPPSDEQLKSGTASVCLLNFPRAKVKQVNDNALQS 180
 D 121 tfgogtkleikrtvaapsvfippsdeqlksgtasvcllnfpreakvkqvdnalqs 180

QY 181 GNSQESVTEQDSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 D 181 gnsqesvteqdsksstyslsltltlskadyekkhkvyacevthqglsspvtksfnrgec 238

RESULT 7
 AAW83033
 ID AAW83033 standard; Protein; 238 AA.
 XX
 AC AAW83033;
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE Anti-Fas humanised antibody HFE7A light chain MM type.
 XX
 KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy.
 XX
 XX Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Peptide 1..20
 FT /label= sig_peptide

FT /label= Mat_protein
 FT 21..131
 FT /label= Variable
 FT 132..238
 FT /label= Constant
 FT 44..58
 FT /label= CDR_L1
 FT /note= "claim 9"
 FT 74..80
 FT /label= CDR_L2
 FT /note= "claim 9"
 FT 113..121
 FT /label= CDR_L3
 FT /note= "claim 9"
 XX AU9859701-A.
 XX 08-OCT-1998.
 XX 30-MAR-1998; 98AU-0059701.
 XX 08-OCT-1997; 97JP-0276064.
 PR 01-APR-1997; 97JP-0082953.
 PR 25-JUN-1997; 97JP-0169088.
 XX (SANY) SANKYO CO LTD.
 PA Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX WPI; 1998-543440/47.
 DR N-PSDB; AAV70077.
 XX New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX Claim 21; Page 218; 292pp; English.
 PS This is the amino acid sequence of the PPHH type humanised light
 XX chain of murine anti-human Fas monoclonal antibody HFE7A.
 CC Humanisation of the murine sequence (see AAW83042) entailed making
 CC D1E, P47A, K49R, H80S, P81R, V82L, E84P, A87E, T89V and R107K
 CC amino acid substitutions; these residues are conserved in the
 CC human light chain (kappa chain). Host cell Escherichia coli
 CC PHSH5 SANK 70398 harbors plasmid PHSH5 carrying a fusion
 CC fragment of the humanised PPHH type HFE7A light chain and DNA
 CC encoding the region of human immunoglobulin kappa chain, and is
 CC deposited as FERM BP-6274 (claimed). The invention provides
 CC methods for producing humanised antibodies by culturing host
 CC cells. Humanised versions of HFE7A (see AAW83031-37), like native
 CC HFE7A, are capable of inducing apoptosis in abnormal cells
 CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal
 CC cells. The humanised antibodies are used to evaluate, in animal
 CC models, treatments of diseases that involve Fas/Fas ligand
 CC interactions, and also to treat such diseases, including autoimmune
 CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
 CC graft versus host disease, Sjogren syndrome, pernicious anaemia,
 CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
 CC sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
 CC thrombopenia purpura and insulin-dependent diabetes), allergies,
 CC atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
 CC nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
 CC rejection (all claimed).
 XX Sequence 238 AA;

Query Match 96.9%; Score 1207; DB 19; Length 238;
 Best Local Similarity 97.5%; Pred. No. 9.3e-65;
 Matches 232; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 METDTILLWVLLWVPGSTGEVETQSPGTLSPGERATLSCKASQSVYDGDSYMNY 60
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 DB 1 metdtillwvllwvpgstge|v|tqspgtlslspperatlsckasqsvdydgdymny 60
 QY 61 QOKFGQAPRLIIYAASNLSEGEEDRFSGSGSGTDFTLIHVPEEEDAAATYYCQNSNEDPR 120
 DQ |||||
 DB 61 qkpgqaprlIIyaasnlesq|gdrfsgsgsgtdftltlsrlepedfavyycqnsnedpr 120
 QY 121 TFGGOTKLEIKRTVAAPSVFTEPDSDEOLKSGTASVWCLLNFFYPREAKVQWKVDNALQS 180
 DQ |||||
 DB 121 tfggotkleikrtvaapsvf|fepdsdeqlksgtasvwc|l|nnfypreakvqwkvdnalqs 180
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 DQ |||||
 DB 181 gnsqsvteqdsksdstys|sls|slk|skadyekhkvyacevthqglsspvtksfnrgec 238
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 AAB14777
 ID AAB14777 standard; Proteins 238 AA.
 AC AAB14777;
 XX 24-NOV-2000 (first entry)
 DE Humanised anti-Fas antibody light chain, SEQ ID NO:107.
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; humanised antibody complementarity determining region; CDR;
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
 KW hepatitis; AIDS; graft rejection; light chain.
 XX Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX JP2000169393-A.
 XX 20-JUN-2000.
 XX 30-SEP-1999; 99JP-0278301.
 XX 30-SEP-1998; 98JP-0276883.
 XX (SANY) SANKYO CO LTD.
 XX WPI; 2000-485645/43.
 DR N-PSDB; AAA72176.
 XX Preventive or treating agent for the diseases caused by an abnormality
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody -
 XX Claim 20; Page 101; 139pp; Japanese.
 XX The invention relates to compositions for the prevention or treatment
 CC or diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The composition of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
 CC represent the light chains of several humanised HFE7A-derived anti-Fas
 CC antibodies.
 XX Sequence 238 AA;

Query Match 96.9%; Score 1207; DB 21; Length 238;
 Best Local Similarity 97.5%; Pred. No. 9.3e-65;
 Matches 232; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 METDTILLWVLLWVPGSTGEIVLTQSPGTLISLSPGERATLSCSKASQSDYDGDYNNWY 60
 DB 1 metdtillwvllwvpgstgeivltqspgtlslsperatlsckasqsdvdygdsymwy 60

QY 61 QOKPGQAPRLIYAASNLSESGIPDRFSGSGGTDFTLTIHPVEEDATYYCQSQNEDPR 120
 DB 61 qkpgqaprllyaaasnlsegsipdrfsgsgsgtdftltisrlepedfavyycqsgnedpr 120

QY 121 TFGOGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQS 180
 DB 121 tfgogtkleikrtvaapsvfifppspdeqlksgtasvvcvllnnfybreakvqkvdnalqs 180

QY 181 GNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 DB 181 gnsqesvteqdsksdystlslstltlskadyekhkvayacevthqglsspvtksfnrgec 238

RESULT 12

AAW90927 standard; Protein: 238 AA.

XX AAW90927;

XX 08-AUG-2000 (first entry)

XX Humanised HFE7A designed light chain protein.

XX Fas: antibody; human: anti-inflammatory; anti-anemic; antidiabetic;
 XX anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
 XX dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 XX nephrotropic; antiinfertility; neuroprotective; antirheumatic; anti-Fas;
 XX hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 XX Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 XX Sjogren's syndrome; anemia; Addison's disease; sterility; myasthenia gravis;
 XX Goodpasture syndrome; Crohn's disease; scleroderma; sterility;
 XX multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 XX insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 XX cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

XX Synthetic.

XX EP990663-A2.

XX 05-APR-2000.

XX 29-SEP-1999; 99EP-0307711.

XX 30-SEP-1998; 98JP-0276881.

XX 30-SEP-1998; 98JP-0276882.

XX (SANY) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

XX WPI; 2000-258930/23.

XX N-PSDB; AAA11614.

XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 XX inflammatory or autoimmune disease, induces apoptosis selectively in
 XX cells with abnormal Fas-Fas ligand systems

XX Claim 3; Page 141-142; 263pp; English.

XX This invention describes a novel humanized anti-Fas antibody-like
 XX molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 XX ligand system, by binding to Fas on the cell surface, and prevents
 XX apoptosis in cells with a normal system, by inhibiting binding between

CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective, induce
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective, induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic) and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A designed light chain which is used in
 CC the method described in the invention.

XX Sequence 238 AA;

Query Match 96.9%; Score 1207; DB 21; Length 238;

Best Local Similarity 97.5%; Pred. No. 9.3e-65;

Matches 232; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 METDTILLWVLLWVPGSTGEIVLTQSPGTLISLSPGERATLSCSKASQSDYDGDYNNWY 60
 DB 1 metdtillwvllwvpgstgeivltqspgtlslsperatlsckasqsdvdygdsymwy 60

QY 61 QOKPGQAPRLIYAASNLSESGIPDRFSGSGGTDFTLTIHPVEEDATYYCQSQNEDPR 120
 DB 61 qkpgqaprllyaaasnlsegsipdrfsgsgsgtdftltisrlepedfavyycqsgnedpr 120

QY 121 TFGOGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQS 180
 DB 121 tfgogtkleikrtvaapsvfifppspdeqlksgtasvvcvllnnfybreakvqkvdnalqs 180

QY 181 GNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 DB 181 gnsqesvteqdsksdystlslstltlskadyekhkvayacevthqglsspvtksfnrgec 238

RESULT 13

AAW83031

ID AAW83031 standard; Protein: 238 AA.

XX AAW83031;

XX 15-MAR-1999 (first entry)

XX Anti-Fas humanised antibody HFE7A light chain HH type.

XX HFE7A: monoclonal antibody; mouse; Fas; humanised antibody;
 XX apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 XX systemic lupus erythematosus; graft versus host disease;
 XX Sjogren syndrome; pernicious anaemia; Addison's disease;
 XX scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 XX rheumatoid arthritis; autoimmune haemolytic anaemia;
 XX myasthenia gravis; multiple sclerosis; Basedow's disease;
 XX thrombopenia purpura; insulin-dependent diabetes; allergy;
 XX atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 XX glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 XX transplant rejection; therapy.

XX Homo sapiens.

XX Synthetic.

XX

FH Key Location/Qualifiers
 FT Peptide 1..20
 FT Protein /label= Sig_peptide
 FT Region 21..238
 FT Region /label= Mat_protein
 FT Region 21..131
 FT Region /label= Variable
 FT Region 132..238
 FT Region /label= Constant
 FT Region 44..58
 FT Region /label= CDR_L1
 FT Region /note= "claim 9"
 FT Region 74..80
 FT Region /label= CDR_L2
 FT Region /note= "claim 9"
 FT Region 113..121
 FT Region /label= CDR_L3
 FT Region /note= "claim 9"
 PN AU9859701-A.
 PD 08-OCT-1998.
 XX 30-MAR-1998; 98AU-0059701.
 XX 08-OCT-1997; 97JP-0276064.
 PR 01-APR-1997; 97JP-0082953.
 PR 25-JUN-1997; 97JP-0169088.
 XX (SANY) SANKYO CO LTD.
 XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX WPI; 1998-543440/47.
 DR N-PSDB; AAV70074.
 XX New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX Claim 21; Page 199-199; 292pp; English.
 XX This is the amino acid sequence of the HH type humanised light
 CC chain of murine anti-human Fas monoclonal antibody HFE7A.
 CC Humanisation of the murine sequence (see AAW83042) entailed making
 CC P47A, K49R, H80S, P81R, V82L, E84P, E85A, A87F and T89V amino acid
 CC substitutions; these residues are conserved in the human light
 CC chain (kappa chain). Host cell Escherichia coli PHSGH7 SANK 73497
 CC harbors plasmid PHSGH7 carrying a fusion fragment of the humanised
 CC HH type HFE7A light chain and DNA encoding the region of human
 CC immunoglobulin kappa chain, and is deposited as FERM BP-6073
 CC (claimed). The invention provides methods for producing humanised
 CC antibodies by culturing host cells. Humanised versions of HFE7A
 CC (see AAW83031-37), like native HFE7A, are capable of inducing
 CC apoptosis in abnormal cells expressing Fas, and of inhibiting
 CC Fas-induced apoptosis in normal cells. The humanised antibodies
 CC are used to evaluate, in animal models, treatments of diseases that
 CC involve Fas/Fas ligand interactions, and also to treat such
 CC diseases, including autoimmune disease (e.g. systemic lupus
 CC erythematosus, Hashimoto's disease, graft versus host disease,
 CC Sjogren syndrome, pernicious anaemia, Addison's disease,
 CC scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid
 CC arthritis, autoimmune haemolytic anaemia, sterility, myasthenia
 CC gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura
 CC and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
 XX Sequence 238 AA;

Query Match 96.0% Score 1195; DB 19; Length 238;
 Best Local Similarity 96.2% Pred. No. 4. 8e-64;
 Matches 229; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 QY 1 METDTILLVLLWVPGSTGSEVLTQSPGTLSLSPGERATLSCASQSYVDYDGSYMNWY 60
 Db |||||
 QY 1 metdtillvlllwvpgstgsevtlqspgtls slsperatlsckasqsydydgsymnw 60
 Db |||||
 QY 61 QOKPGQAPRLIYAASNLSEGRDRFSGSGCTDFTLTTHPVEEEDAATYCCOOSNEDPR 120
 Db |||||
 QY 61 gqpggaprlliyaasnlesgdrfsgsgsgtdftltisrlpadfavyvqqsqnedpr 120
 Db |||||
 QY 121 TFGQGTKEIKRTVAAPSVFIFEPSSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQS 180
 Db |||||
 QY 121 tfgqgtrleikrtvaapsvfifepssdeqlksgtasvclnnfypreakvqkvdnalqs 180
 Db |||||
 QY 181 GNSQSVTEQDSKSTYSLSSDTLSKADYKHKYVACEVTHOGLSSPVTKSFNRGEC 238
 Db |||||
 QY 181 gnsqsvteqdsksstyslsstlskadyekhkvacevthogllsspvtksfnrgec 238
 Db |||||
 RESULT 14
 AAB14772
 ID AAB14772 standard; Protein# 238 AA.
 XX AC AAB14772;
 XX DT 24-NOV-2000 (first entry)
 XX DE Humanised anti-Fas antibody light chain, SEQ ID NO:50.
 XX KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; humanised antibody complementarity determining region; CDR;
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
 KW hepatitis; AIDS; graft rejection; light chain.
 XX OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX JP2000169393-A.
 XX PD 20-JUN-2000.
 XX PF 30-SEP-1999; 99JP-0278305.
 XX PR 30-SEP-1998; 98JP-0276886.
 XX PA (SANY) SANKYO CO LTD.
 XX WPI; 2000-485645/43.
 DR N-PSDB; AAA72124.
 XX Preventive or treating agent for the diseases caused by an abnormality
 in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 anti-Fas antibody
 PS Claim 20; Page 78-79; 139pp; Japanese.
 XX The invention relates to compositions for the prevention or treatment
 or diseases caused by an abnormality in the Fas/Fas ligand system
 containing an anti-Fas antibody as the active component. The anti-Fas
 antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 or a humanised version of HFE7A containing identical CDRs
 (complementarity determining regions) to antibody HFE7A. Via its
 interaction with Fas, the antibody of the invention acts as a modulator
 of apoptosis. The compositions of the invention may therefore be used in
 the treatment or prevention of conditions such as autoimmune diseases,
 allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
 represent the light chains of several humanised HFE7A-derived anti-Fas

CC antibodies.

XX
SQ Sequence 238 AA;

Query Match 96.08; Score 1195; DB 21; Length 238;
 Best Local Similarity 96.24; Pred. No. 4.8e-64;
 Matches 229; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 METDTILLWLLWVPGSTGEIVLTQSPGTLISLSPGERATLSCRKASQSDVDYDGSYNNWY 60
 DB 1 metdtillwllwvpgstgdvltqspgtlslspsgeratlsckasqsdvdydgsymnw 60
 QY 61 QOKPGQAPRLIYAASNLESGIPDRFSGSGGTDFTLTIHPVEEDAAATYYCQSQNEDPR 120
 DB 61 qkpgqaprllyaaasnlesgipdrfsgsgsgtdftltisrlepadvfayycqsgnedpr 120
 QY 121 TFGGOTKLEIKRTVAAPSVFIPTPPDEOLKSGTASVCLLNFFYPRAKQVQKVDNALQS 180
 DB 121 tfgggtlrleikrtvaapsvfippsdeqlksgtasvcllnffypreakvqkvdnalqs 180
 QY 181 GNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 DB 181 gnsqesvteqdsksdystltsltskadyekhkvyacevthqglsspvtksfnrgec 238

RESULT 15

AAW90922
ID AAW90922 standard; Protein; 238 AA.

AC AAW90922;

XX
DT 08-AUG-2000 (first entry)

XX Humanised anti-Fas antibody HFE7A light chain HH type protein.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotection; antilarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

XX Synthetic.

XX EP990663-A2.

XX

XX 05-APR-2000.

XX 29-SEP-1999; 99EP-0307711.

XX 30-SEP-1998; 98JP-0276881.

XX 30-SEP-1998; 98JP-0276882.

XX (SANY) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

XX WPI; 2000-258930/23.

XX N-PSDB; AAA11562.

XX

XX New humanized anti-Fas antibody, useful for treating or preventing e.g.

XX inflammatory or autoimmune disease, induces apoptosis selectively in

XX cells with abnormal Fas-Fas ligand systems

XX Example reference 14; Page 114-115; 263pp; English.

XX This invention describes a novel humanized anti-Fas antibody-like

CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antilarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A light chain HH type which is used in
 CC the method described in the invention.

XX SQ Sequence 238 AA;

Query Match

Best Local Similarity 96.08; Score 1195; DB 21; Length 238;

Matches 229; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 METDTILLWLLWVPGSTGEIVLTQSPGTLISLSPGERATLSCRKASQSDVDYDGSYNNWY 60

DB 1 metdtillwllwvpgstgdvltqspgtlslspsgeratlsckasqsdvdydgsymnw 60

QY 61 QOKPGQAPRLIYAASNLESGIPDRFSGSGGTDFTLTIHPVEEDAAATYYCQSQNEDPR 120

DB 61 qkpgqaprllyaaasnlesgipdrfsgsgsgtdftltisrlepadvfayycqsgnedpr 120

QY 121 TFGGOTKLEIKRTVAAPSVFIPTPPDEOLKSGTASVCLLNFFYPRAKQVQKVDNALQS 180

DB 121 tfgggtlrleikrtvaapsvfippsdeqlksgtasvcllnffypreakvqkvdnalqs 180

QY 181 GNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238

DB 181 gnsqesvteqdsksdystltsltskadyekhkvyacevthqglsspvtksfnrgec 238

Search completed: April 24, 2002, 15:09:54

Job time: 97 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 15:10:42 ; Search time 42.08 Seconds
(without alignments)
127.276 Million cell updates/sec

Title: US-09-499-662-109

Perfect score: 1245

Sequence: 1 METDTILLWLLWVPGSTG.....EVTHOGLSPVTKFSNRGEC 238

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1031	82.8	218	5	PCT-US96-13152-2
2	1017	81.7	218	2	US-08-887-352B-13
3	1017	81.7	218	3	US-08-466-151-9
4	1017	81.7	218	4	US-09-109-207C-13
5	1017	81.7	218	4	US-09-296-005-13
6	994	79.8	218	4	US-09-282-505-1
7	994	79.8	218	4	US-09-054-255-1
8	991	79.6	218	2	US-08-887-352B-15
9	991	79.6	218	2	US-08-887-352B-17
10	991	79.6	218	2	US-08-887-352B-19
11	991	79.6	218	2	US-08-887-352B-24
12	991	79.6	218	4	US-09-109-207C-15
13	991	79.6	218	4	US-09-109-207C-17
14	991	79.6	218	4	US-09-109-207C-19
15	991	79.6	218	4	US-09-109-207C-24
16	991	79.6	218	4	US-09-296-005-15
17	991	79.6	218	4	US-09-296-005-17
18	991	79.6	218	4	US-09-296-005-19
19	991	79.6	218	4	US-09-296-005-24
20	971.5	78.0	239	3	US-08-487-550-6
21	968.5	77.8	241	2	US-07-916-098A-56
22	959	77.0	234	4	US-09-049-672A-6
23	945.5	75.9	235	4	US-09-171-945-97
24	941.5	75.6	235	1	US-08-276-852-153
25	941.5	75.6	235	1	US-08-899-575-153
26	941.5	75.6	235	1	US-08-899-575-153
27	941.5	75.6	235	5	PCT-US95-08743-153

28	939.5	75.5	233	2	US-07-934-373C-25
29	939.5	75.5	233	3	US-08-437-642B-25
30	939.5	75.5	233	5	PCT-US93-07832-25
31	936	75.2	214	2	US-07-934-373C-39
32	936	75.2	214	3	US-08-437-642B-39
33	936	75.2	214	5	PCT-US93-07832-39
34	931.5	74.8	235	4	US-09-171-945-99
35	931	74.8	214	2	US-07-934-373C-40
36	931	74.8	214	3	US-08-788-800-11
37	931	74.8	214	3	US-08-437-642B-40
38	931	74.8	214	3	US-09-097-309-2
39	931	74.8	214	4	US-09-097-171A-2
40	931	74.8	214	5	PCT-US93-07832-40
41	931	74.8	237	3	US-09-097-309-6
42	931	74.8	237	4	US-09-097-171A-10
43	931	74.8	237	4	US-09-422-712B-2
44	931	74.8	237	4	US-09-607-756-2
45	930.5	74.7	235	4	US-09-171-945-52

ALIGNMENTS

RESULT 1

PCT-US96-13152-2

; Sequence 2, Application PC/TUS9613152

; GENERAL INFORMATION:

; APPLICANT: Martin, Ulrich et al.

; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felfe & Lynch

; ADDRESSEE: Attn: Norman D. Hanson

; STREET: 805 Third Avenue

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Computer Disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/13152

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/578,953

; FILING DATE: 27-Dec-95

; APPLICATION NUMBER: EP 95 112 895.8

; FILING DATE: 17-Aug-95

; APPLICATION NUMBER: EP 95 114 969.9

; FILING DATE: 19-Sep-95

; ATTORNEY/AGENT INFORMATION:

; NAME: Norman D. Hanson

; REGISTRATION NUMBER: 30 8946

; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH

; TELEPHONE: (212) 688-9200

; TELEPHONE: (212) 838-3884

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 218

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; PCT-US96-13152-2

Query Match

Best Local Similarity

82.8%

Score 1031; DB 5;

Length 218;

Pred. No. 5.6e-81;

QY 141 IFPPDEQLKSGTASVYVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYSL 200
Db 121 IFPPDEQLKSGTASVYVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
QY 201 STLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238
Db 181 STLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 218

RESULT 4
US-09-109-207C-13
; Sequence 13, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123r1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-13

Query Match 81.7%; Score 1017; DB 4; Length 218;
Best Local Similarity 88.5%; Pred. No. 8.8e-80;
Matches 193; Conservative 13; Mismatches 12; Indels 0; Gaps 0;
QY 21 EIVLTQSPGTLSPGERATLSCASQSYVDYDGSYNNWYQKPGQAPRLIIYAASNLES 80
Db 1 DIQLTQSPSSLASVGRVTITCRASQSYVDYDGSYNNWYQKPGKAPKLLIIYAASYLE 60
QY 81 GIPDRFSGSGSDFTLTITHPVEEEDAATYYCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
Db 61 GVPDRFSGSGSDFTLTITSSLPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
QY 141 IFPPDEQLKSGTASVYVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYSL 200
Db 121 IFPPDEQLKSGTASVYVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
QY 201 STLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238
Db 181 STLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 218

RESULT 5
US-09-296-005-13
; Sequence 13, Application US/09296005
; Patent No. 6250957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial

; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-296-005-13

Query Match 81.7%; Score 1017; DB 4; Length 218;
Best Local Similarity 88.5%; Pred. No. 8.8e-80;
Matches 193; Conservative 13; Mismatches 12; Indels 0; Gaps 0;
QY 21 EIVLTQSPGTLSPGERATLSCASQSYVDYDGSYNNWYQKPGQAPRLIIYAASNLES 80
Db 1 DIQLTQSPSSLASVGRVTITCRASQSYVDYDGSYNNWYQKPGKAPKLLIIYAASYLE 60
QY 81 GIPDRFSGSGSDFTLTITHPVEEEDAATYYCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
Db 61 GVPDRFSGSGSDFTLTITSSLPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
QY 141 IFPPDEQLKSGTASVYVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYSL 200
Db 121 IFPPDEQLKSGTASVYVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
QY 201 STLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238
Db 181 STLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 218

RESULT 6
US-09-282-505-1
; Sequence 1, Application US/09282505A
; Patent No. 6194551
; GENERAL INFORMATION:
; APPLICANT: Eschoe Ekinaduese Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R1
; CURRENT APPLICATION NUMBER: US/09/282,505A
; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-218
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6194551
US-09-282-505-1

Query Match 79.8%; Score 994; DB 4; Length 218;
Best Local Similarity 86.7%; Pred. No. 8.2e-78;
Matches 189; Conservative 15; Mismatches 14; Indels 0; Gaps 0;
QY 21 EIVLTQSPGTLSPGERATLSCASQSYVDYDGSYNNWYQKPGQAPRLIIYAASNLES 80
Db 1 DIQLTQSPSSLASVGRVTITCRASQSYVDYDGSYNNWYQKPGKAPKLLIIYAASYLE 60
QY 81 GIPDRFSGSGSDFTLTITHPVEEEDAATYYCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
Db 61 GVPDRFSGSGSDFTLTITSSLPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
QY 141 IFPPDEQLKSGTASVYVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYSL 200
Db 121 IFPPDEQLKSGTASVYVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
QY 201 STLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238
Db 181 STLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 218

RESULT 7
US-09-054-255-1
; Sequence 1, Application US/09054255

```
; Patent No. 6242195
; GENERAL INFORMATION:
; APPLICANT: Esche Ekinaduse Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266
; CURRENT APPLICATION NUMBER: US/09/054,255
; CURRENT FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: E27 anti-IgE antibody light chain
US-09-054-255-1

Query Match          79.8%      Score 994; DB 4; Length 218;
Best Local Similarity 86.7%; Pred. No. 8.2e-76;
Matches 189; Conservative 15; Mismatches 14; Indels 0; Gaps 0;

QY 21 EIVLTQSPGTLSPGERATLSCASQSDVDYDGDSDYNNYQOKPGQAPRLIIYAASNLES 80
DB 1 DIQLTQSPSSLASVGDRTVITCRASKPVDGEGSYNNYQOKPGKAPKLLIIYAASYLES 60
QY 81 GIPDRFSGSGGTFTLTTHPVEEDDAATYYCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
DB 61 GVPDRFSGSGGTFTLTTHPVEEDDAATYYCQSNEDPRTFGQGTKEIKRTVAAPSVF 120
QY 141 IFPPSDEQLKSGTASVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYLS 200
DB 121 IFPPSDEQLKSGTASVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
QY 201 STLTSLKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 238
DB 181 STLTSLKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 218

RESULT 8
US-08-887-352B-15
; Sequence 15, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acids
; TOPOLOGY: Linear
US-08-887-352B-15
```

```
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-15

Query Match          79.6%      Score 991; DB 2; Length 218;
Best Local Similarity 86.2%; Pred. No. 1.5e-77;
Matches 188; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 21 EIVLTQSPGTLSPGERATLSCASQSDVDYDGDSDYNNYQOKPGQAPRLIIYAASNLES 80
DB 1 DIQLTQSPSSLASVGDRTVITCRASKPVDGEGSYNNYQOKPGKAPKLLIIYAASYLES 60
QY 81 GIPDRFSGSGGTFTLTTHPVEEDDAATYYCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
DB 61 GVPDRFSGSGGTFTLTTHPVEEDDAATYYCQSNEDPRTFGQGTKEIKRTVAAPSVF 120
QY 141 IFPPSDEQLKSGTASVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYLS 200
DB 121 IFPPSDEQLKSGTASVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
QY 201 STLTSLKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 238
DB 181 STLTSLKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 218

RESULT 9
US-08-887-352B-17
; Sequence 17, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-17

Query Match          79.6%      Score 991; DB 2; Length 218;
Best Local Similarity 86.2%; Pred. No. 1.5e-77;
Matches 188; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 21 EIVLTQSPGTLSPGERATLSCASQSDVDYDGDSDYNNYQOKPGQAPRLIIYAASNLES 80
DB 1 DIQLTQSPSSLASVGDRTVITCRASKPVDGEGSYNNYQOKPGKAPKLLIIYAASYLES 60
```


US-09-109-207C-24

Query Match 79.6%; Score 991; DB 4; Length 218;
Best Local Similarity 86.2%; Pred. No. 1.5e-77;
Matches 188; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

Qy	21	EIVLTQSPGTLSPGERATLSCRASQSVYDGDSDSYMNYOQKPGQAPRLIIYAASNLES	80
Db	1	DIQLTQSPSLASVGDRTITCRASKPVDGEGSYLNNYQKPGKAPKLLIYAASYLE	60
Qy	81	GIPDRFSGSGCTDFTLTTHPVEEEDATYYCQOSNEDPRTFGGQTKLEIKRTVAAPSVF	140
Db	61	GVPSRFSGSGSDFTLTLSLQPEDFATYYCQOSHEDPYTFGGQTKVEIKRTVAAPSVF	120
Qy	141	IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS	200
Db	121	IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS	180
Qy	201	STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	238
Db	181	STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	218

Search completed: April 24, 2002, 15:10:42
Job time: 145 sec



F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 933.5; DB 2; Length 215;
Best Local Similarity 84.9%; Pred. No. 1.2e-53;
Matches 186; Conservative 8; Mismatches 20; Indels 5; Gaps 2;

Qy 21 EIVLTQSPGTLSPGERATLSCASQSDYDGDSDYMMWYQKPGQAPRLIIYAASNLES 80
I:||||| |||:|||||:||||| I: |||:||||| |||: |||:
Db 1 EIVLTQSPATLSVSPGERATLSCRASQSV----HSLAWYQKPGQAPRLIIYRASTRAT 56
Qy 81 GIPDRFSGSGGTDFTLTHPVEEDAATYYCQSQNE-DPRFTGGQGTKEIKRTVAAPSV 139
||| |||:||||| |||: ||| |||: ||| |||: ||| |||: ||| |||:
Db 57 GIPARFSGSGGTDFTLTISLSQSEDFALYYCQYNTWPLTFGGGTKEIKRTVAAPSV 116
Qy 140 IFPPSDQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 199
||||| |||:||||| |||: ||| |||: ||| |||: ||| |||: ||| |||:
Db 117 IFPPSDQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 176
Qy 200 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
||||| |||:||||| |||: ||| |||: ||| |||: ||| |||: ||| |||:
Db 177 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215

RESULT 3
JE0243
Ig kappa chain NIG93 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0243
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazl, H.; T
submitted to JIPID, November 1998
A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
A:Reference number: JE0243
A:Accession: JE0243
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 73.0%; Score 908.5; DB 2; Length 215;
Best Local Similarity 82.6%; Pred. No. 5e-52;
Matches 181; Conservative 12; Mismatches 21; Indels 5; Gaps 2;

Qy 21 EIVLTQSPGTLSPGERATLSCASQSDYDGDSDYMMWYQKPGQAPRLIIYAASNLES 80
I:||||| |||:|||||:||||| : ||| |||: ||| |||: ||| |||:
Db 1 EIVLTQSPATLSVSPGERATLSCRASQSV---ATNVVWYQKPGQAPRLIIYDASTRAT 56
Qy 81 GIPDRFSGSGGTDFTLTHPVEEDAATYYCQSQNE-DPRFTGGQGTKEIK-RTVAAPSV 139
I: |||:|||||:||||| : ||| |||: ||| |||: ||| |||: ||| |||:
Db 57 GIPARFSGSGGTDFTLTISLSQSEDFALYYCQHNNAPWPTFGGTKEIKRTVAAPSV 116
Qy 140 IFPPSDQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 199
||||| |||:||||| |||: ||| |||: ||| |||: ||| |||: ||| |||:
Db 117 IFPPSDQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 176
Qy 200 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
||||| |||:||||| |||: ||| |||: ||| |||: ||| |||: ||| |||:
Db 177 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215

RESULT 4
A23746
Ig kappa chain V-III (KAU cold agglutinin) - human
C:Species: Homo sapiens (man)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C:Accession: A23746
R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl
A:Reference number: A23746; MUID:91131575
A:Accession: A23746

A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-215 <LEO>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 72.8%; Score 906.5; DB 2; Length 215;
Best Local Similarity 85.3%; Pred. No. 6.8e-52;
Matches 185; Conservative 6; Mismatches 23; Indels 3; Gaps 1;

Qy 21 EIVLTQSPGTLSPGERATLSCASQSDYDGDSDYMMWYQKPGQAPRLIIYAASNLES 80
||||| |||:||||| |||: ||| |||: ||| |||: ||| |||: ||| |||:
Db 1 EIVLTQSPATLSVSPGERATLSCASQSV---SSNYLAWYQKPGQAPRLIIYDASSRAT 57
Qy 81 GIPDRFSGSGGTDFTLTHPVEEDAATYYCQSQNE-DPRFTGGQGTKEIKRTVAAPSV 140
||||| |||:||||| |||: ||| |||: ||| |||: ||| |||: ||| |||:
Db 58 GIPDRFSGSGGTDFTLTISREPEDFAVYQYGGSSPLTFGGGTKEIKRTVAAPSV 117
Qy 141 IFPPSDQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 200
||||| |||:||||| |||: ||| |||: ||| |||: ||| |||: ||| |||:
Db 118 IFPPSDQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 177
Qy 201 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGE 237
||||| |||:||||| |||: ||| |||: ||| |||: ||| |||: ||| |||:
Db 178 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGE 214

RESULT 5
JE0241
Ig kappa chain Am37 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0241
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda
submitted to JIPID, November 1998
A:Description: Structure relationship of kappa type light chains with AL amyloidosis:
A:Reference number: JE0241
A:Accession: JE0241
A:Molecule type: protein
A:Residues: 1-216 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-92/Domain: immunoglobulin homology <IMM>

Query Match 70.0%; Score 871; DB 2; Length 216;
Best Local Similarity 78.9%; Pred. No. 1.3e-49;
Matches 172; Conservative 18; Mismatches 26; Indels 2; Gaps 2;

Qy 21 EIVLTQSPGTLSPGERATLSCASQSDYDGDSDYMMWYQKPGQAPRLIIYAASNLES 80
I:||||| |||:|||||:||||| : ||| |||: ||| |||: ||| |||: ||| |||:
Db 1 DIVLTQSPDFLAVSLGERATLSCASQSVLYNSKFNFLAWYQKPGQ-PKLLIW-ANVRES 58
Qy 81 GIPDRFSGSGGTDFTLTHPVEEDAATYYCQSQNE-DPRFTGGQGTKEIKRTVAAPSV 140
I: ||| |||: ||| |||: ||| |||: ||| |||: ||| |||: ||| |||:
Db 59 GVPDRFRSGSGGTDFTLTISNLQAEVLAVYVYQYVSTPYSFGGGRLEIKRTVAAPSV 118
Qy 141 IFPPSDQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 200
||||| |||:||||| |||: ||| |||: ||| |||: ||| |||: ||| |||:
Db 119 IFPPSDQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 178
Qy 201 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
||||| |||:||||| |||: ||| |||: ||| |||: ||| |||: ||| |||:
Db 179 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 216

RESULT 6
S06084
Ig kappa chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S06084

R;Crowe, J.S.; Smith, M.A.; Cooper, H.J.

Nucleic Acids Res. 17, 7992, 1989

A;Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA

A;Reference number: S06084; MUID:90016888

A;Accession: S06084

A;Molecule type: mRNA

A;Residues: 1-240 <CRO>

A;Cross-references: EMBL:X16129; NID:g56457; PIDN:CAA34256.1; PID:g56458

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-240/Product: Ig kappa chain #status predicted <MAT>

F;153-222/Domain: immunoglobulin homology <IMM>

Query Match 63.8%; Score 794; DB 2; Length 240;

Best Local Similarity 62.5%; Pred. No. 1.4e-44;

Matches 150; Conservative 35; Mismatches 53; Indels 2; Gaps 1;

QY 1 MEYDITLLWLLVWPGSTGEIVLTQSPGTLSPGERATLSCASQSDYDGD--SYMN 58

Db 1 MESQTVLMSLLWISGTCGDFVMTQSPSLAVSAGETVITNCKSSQSLFVSGNQKNLA 60

QY 59 WYQKPGQAPRLLIYAASNLGSGIPDRFSGSGCTDFTLHPVEEEDATYYCQSQNSD 118

Db 61 WYQKPGQAPRLLIYAASNLGSGIPDRFSGSGCTDFTLHPVEEEDATYYCQSQNSD 120

QY 119 PRFGQGTLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRKAKVQKVDNAL 178

Db 121 PYTFGAGTKLELRADAAPTVSIFPPSDEQLKSGTASVCLLNNFYPRKAKVQKVDNAL 180

QY 179 QSGNSQESVTEQDSKDSYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238

Db 181 RRDGLDSVTDQDSKDSYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 7

S68241

Ig kappa chain V region (Mab13-1) - mouse (fragment)

N;Alternate names: immunoglobulin light chain

C;Species: Mus musculus (house mouse)

C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000

R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.

submitted to the EMBL data Library, March 1994

A;Description: Specific peroxidase activity by formation of an antibody L-chain-porphyrin

A;Reference number: S68241

A;Accession: S68241

A;Molecule type: mRNA

A;Residues: 1-218 <TAK>

A;Cross-references: EMBL:D29670; NID:g473962; PIDN:BAA06141.1; PID:g473963

R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.

FEBS Lett. 375, 273-276, 1995

A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin

A;Reference number: S68211; MUID:96085223

A;Accession: S68214

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 'NI', 3-212 <TAW>

A;Cross-references: EMBL:D29670

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

Query Match 62.8%; Score 782; DB 2; Length 218;

Best Local Similarity 67.0%; Pred. No. 7.3e-44;

Matches 146; Conservative 28; Mismatches 44; Indels 0; Gaps 0;

QY 21 EIVLTQSPGTLSPGERATLSCASQSDYDGDSDYNNVYQKPGQAPRLLIYAASNL 80

Db 1 ELVLTQSPASLAVSLGORATISCRASKSVASGYIYHWYQKPGQAPRLLIYAASNL 60

QY 81 GIPDRFSGSGSGTDFTLTTHPVEEEDATYYCQSQNSDPRFTFGQGTLEIKRTVAAPSVF 140

Db 61 GVPARFSGSGSGTDFTLTTHPVEEEDATYYCQHSRELPLTFGAGTKLELRADAAPT 120

QY 141 IFPPSDEQLKSGTASVCLLNNFYPRKAKVQKVDNALQSGNSQESVTEQDSKDSYSL 200

Db 121 IFPPSDEQLKSGTASVCLLNNFYPRKAKVQKVDNALQSGNSQESVTEQDSKDSYSL 180

QY 201 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238

Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 8

JC5810

monoclonal antibody 13-1 light chain - mouse

C;Species: Mus musculus (house mouse)

C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000

A;Accession: JC5810

R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada,

Biochem. Biophys. Res. Commun. 240, 566-572, 1997

A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a por-

A;Reference number: JC5810; MUID:98063277

A;Accession: JC5810

A;Molecule type: protein

A;Residues: 1-218 <AKA>

C;Comment: This catalytic antibody has peroxidase oxidase. It is directed against a

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-94/Domain: immunoglobulin homology <IMM>

Query Match 62.3%; Score 776; DB 2; Length 218;

Best Local Similarity 67.3%; Pred. No. 1.8e-43;

Matches 146; Conservative 26; Mismatches 45; Indels 0; Gaps 0;

QY 22 IVLTQSPGTLSPGERATLSCASQSDYDGDSDYNNVYQKPGQAPRLLIYAASNL 81

Db 2 IVLTQSPASLAVSLGORATISCRASKSVASGYIYHWYQKPGQAPRLLIYAASNL 61

QY 82 IPDRFSGSGSGTDFTLTTHPVEEEDATYYCQSQNSDPRFTFGQGTLEIKRTVAAPSV 141

Db 62 VPARFSGSGSGTDFTLTTHPVEEEDATYYCQHSRELPLTFGAGTKLELRADAAPT 121

QY 142 FPPSDEQLKSGTASVCLLNNFYPRKAKVQKVDNALQSGNSQESVTEQDSKDSYSL 201

Db 122 FPPSDEQLKSGTASVCLLNNFYPRKAKVQKVDNALQSGNSQESVTEQDSKDSYSL 181

QY 202 TLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238

Db 182 TLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 9

A56169

Ig kappa chain V region (clone 23.2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jan-2000

A;Accession: A56169

R;Montardini, C.; Kieber-Emmons, T.; VonFeldt, J.M.; O'Malley, B.; Rosenbaum, H.; Go

J. Biol. Chem. 270, 6628-6638, 1995

A;Title: Recombinant antibodies in bioactive peptide design.

A;Reference number: A56169; MUID:95204454

A;Accession: A56169

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-210 <MON>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 60.4%; Score 752; DB 2; Length 210;

Best Local Similarity 67.5%; Pred. No. 6.1e-42;

Matches 141; Conservative 28; Mismatches 40; Indels 0; Gaps 0;

QY 21 EIVLTQSPGTLSPGERATLSCASQSYVDYDGDSDYNNYQKPGQAPRLIIYAASNL 80
Db 1 DIVLTQSPASLTIVSLGQATISCRASKSYSGSYMMHWYQKPGQPKVLIYASNL 60

QY 81 GIPDFSGSGSDTFTLIHPVEEDAATYYCQSQNEDPRFQGTGKLEIKRTVAAPSVF 140
Db 61 GVPFSGSGSDTFTLIHPVEEDAATYYCOHSRELPTWFGGTRLEIKRADAPTVS 120

QY 141 IPPPSDEQLKSGTASVCLLNFFYPREAKVQKVDNALQSGNSQSVTEQDSKSTYS 200
Db 121 IPPPSSEQLTSGGASVCLLNFFYPKIDNVKWKIDGSRQNGVLNSWTDDQDSKSTYS 180

QY 201 STLTLSKADYKHKVYACEVTHQGLSSPV 229
Db 181 STLTTLTKDEYERHNSYTCETHKTSTSPI 209

RESULT 10
A31790
Ig kappa chain V region (17/9) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: A31790
R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an
A:Reference number: A92686; MUID:89034213
A:Accession: A31790
A:Molecule type: mRNA
A:Residues: 1-220 <SCH>
A:Cross-references: GB:M23626; GB:J04061; NID:9533234; PIDN:AAA39162.1; PID:g533235
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 57.5%; Score 716; DB 2; Length 220;
Best Local Similarity 60.5%; Pred. No. 1.3e-39;
Matches 133; Conservative 34; Mismatches 51; Indels 2; Gaps 1;

QY 21 EIVLTQSPGTLSPGERATLSCASQSYVDG--DSVMNYYQKPGQAPRLIIYAASNL 78
Db 1 DIVMTQSPSLTIVAGKVTVMSCSSQSLFNSGKQKYLTYWYQKPGQPKVLIYASTR 60

QY 79 ESGIPDFSGSGSDTFTLIHPVEEDAATYYCQSQNEDPRTEGQGTLEIKRTVAAPS 138
Db 61 ESGVPDFSGSGSDTFTLISSVQAEADLAYVCQNDYNSPLTFGGTGKLEIKRADAPT 120

QY 139 VFIPPSDEQLKSGTASVCLLNFFYPREAKVQKVDNALQSGNSQSVTEQDSKSTYS 198
Db 121 VSIFPPSSEQLTSGGASVCLLNFFYPKIDNVKWKIDGSRQNGVLNSWTDDQDSKSTYS 180

QY 199 LSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 MSSTLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNRNEC 220

RESULT 11
S14237
Ig kappa chain precursor (15C5) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S14237
R:Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.
Eur. J. Biochem. 192, 767-775, 1990
A:Title: Construction and characterization of a recombinant murine monoclonal antibody
A:Reference number: S14236; MUID:91006173
A:Accession: S14237
A:Molecule type: mRNA
A:Residues: 1-234 <VNA>
A:Cross-references: EMBL:X56394; NID:951622; PIDN:CAA39805.1; PID:g51623
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 57.2%; Score 712; DB 2; Length 234;
Best Local Similarity 56.3%; Pred. No. 2.6e-39;
Matches 134; Conservative 37; Mismatches 63; Indels 4; Gaps 1;

QY 1 METDTILLVLLWVPGSTGEIVLTQSPGTLSPGERATLSCASQSYVDYDGDSDYNNY 60
Db 1 MRTPAQFLGILLWPPGKCDKMTQSPSSMVASLGERVTVTCASQDI---NSYLSWI 56

QY 61 QOKFQAPRLIIYAASNLSEGIIPDFSGSGSDTFTLIHPVEEDAATYYCQSQNEDPR 120
Db 57 QOKPKSPKTLIYRGNRLVAGVPSRFSGSGGQDYSLTSSLEYDGVGYVYCLRYDEPFF 116

QY 121 TFGGTGKLEIKRTVAAPSVTEPPSPDEQLKSGTASVCLLNFFYPREAKVQKVDNALQ 180
Db 117 TFGSGTKLEIKRADAPTSTPEPPSSEQLTSGGASVCLLNFFYPKIDNVKWKIDGSRQ 176

QY 181 GNSQESVTEQDSKSTYSLSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 177 NGVLNSWTDDQDSKSTYSMSSTLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNRNEC 234

RESULT 12
S33161
Ig kappa chain - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C:Accession: S33161
R:Foley, R.C.; Beh, K.J.
submitted to the EMBL Data Library, July 1990
A:Description: Isolation and characterisation of sheep kappa light chain cDNA.
A:Reference number: S33161
A:Accession: S33161
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-230 <FOL>
A:Cross-references: EMBL:X54110; NID:g297103; PIDN:CAA38046.1; PID:g1364221
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:143-212/Domain: immunoglobulin homology <IMM>

Query Match 56.9%; Score 708.5; DB 2; Length 230;
Best Local Similarity 57.9%; Pred. No. 4.3e-39;
Matches 133; Conservative 39; Mismatches 54; Indels 5; Gaps 2;

QY 7 LLWVLLW-VPGSTGEIVLTQSPGTLSPGERATLSCASQSYVDYDGDSDYNNYQKPG 65
Db 2 LLGILLWLLPGARCDIQVTPSPSSLSALUTERVSICTRTSQSV---SNLYNYYQKPG 57

QY 66 QAPRLIIYAASNLSEGIIPDFSGSGSDTFTLIHPVEEDAATYYCQSQNEDPRTEGQ 125
Db 58 QAPKLLIYYATRLTHTDVPSPFSGSGSDTFTLTISLEANDTATYVYCLQVESTPLAFEGG 117

QY 126 TKLEIKRTVAAPSVTEPPSPDEQLKSGTASVCLLNFFYPREAKVQKVDNALQSGNSQ 185
Db 118 TNVEIKRSDAQSPVFLFKPSEQLRTGTSVSVCLVNDYFPKIDNVKWKIDGVTGNSFQN 177

QY 186 SVTEQDSKSTYSLSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 178 SFTDDQSKSTYSLSLTLSSEIYQSHNAYACEVSHKSLPTALVKSFNRNEC 230

RESULT 13
PC4203
Ig kappa chain (monoclonal antibody MabA34) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C:Accession: PC4203
R:Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996

A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a mAb
A;Reference number: PC4202; MUID:97082978

A;Accession: PC4203

A;Molecule type: mRNA

A;Residues: 1-219 <KIP>

A;Cross-references: GB:U29147; NID:g1594225; PIDN:AA52821.1; PID:g1594226

C;Comment: This protein is specific for human plasma apolipoprotein A-I of high-density

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;1-112/Domain: V region #status predicted <VRG>

F;113-219/Domain: C region #status predicted <CRG>

Query Match 56.7%; Score 706.5; DB 2; Length 219;

Best Local Similarity 59.8%; Pred. No. 5.5e-39;

Matches 131; Conservative 38; Mismatches 49; Indels 1; Gaps 1;

QY 21 EIVLTQSPGTLSPGERATLSCASQSDY-DGDSYNNYQOKPGOAPRLIIYAASNLE 79

DB 1 DVLMTQPLSLPVSGLGQASISCRSSQSIHTNGNTLYLEWYLOKPGOSPKLLIYKVSNR 60

QY 80 SGIPDRFSGSGGTDFLTTHPVEEADAATYYCOQSNEDPRTFGQGTKEIKRTVAAPSV 139

DB 61 SGVPDRFSGSGGTDFLTISRVEAEDLGYFCFGSHVPTFGGGTKLEIKRADAAPT 120

QY 140 FIPPPDEQLKSGTASVYVCLLNFPYREKAVQKVDNALQSGNSQESVTEQDSKDSYSL 199

DB 121 SIFFPSSEQLTSGGASVVCFLNFPYKIDINVKWKIDGSRQNGVLNSWTDQDSKDSYSL 180

QY 200 SSTLTSLKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 238

DB 181 SSTLTSLKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 219

RESULT 14

S38865

Ig kappa chain - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar-2001

C;Accession: S38865

R;Kipp, B.; Becker, W.; Schlaak, M.

submitted to the EMBL Data Library, November 1993

A;Description: Combination of a defined specificity and desired isotype by cloning of an

A;Reference number: S38864

A;Accession: S38865

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-219 <KIP>

A;Cross-references: EMBL:227396; NID:g416538; PIDN:CAA81787.1; PID:g416539

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

Query Match

Best Local Similarity 61.2%; Pred. No. 5.5e-39;

Matches 134; Conservative 34; Mismatches 50; Indels 1; Gaps 1;

QY 21 EIVLTQSPGTLSPGERATLSCASQSDY-DGDSYNNYQOKPGOAPRLIIYAASNLE 79

DB 1 ELVMTQPLSLPVSGLGQASISCRSSQSIHTNGNTLYLHWYLOKPGOSPKLLIYIVSNR 60

QY 80 SGIPDRFSGSGGTDFLTTHPVEEADAATYYCOQSNEDPRTFGQGTKEIKRTVAAPSV 139

DB 61 SGVPDRFSGSGGTDFLTISRVEAEDLGYFCFGSHVPTFGGGTKLEIKRADAAPT 120

QY 140 FIPPPDEQLKSGTASVYVCLLNFPYREKAVQKVDNALQSGNSQESVTEQDSKDSYSL 199

DB 121 SIFFPSSEQLTSGGASVVCFLNFPYKIDINVKWKIDGSRQNGVLNSWTDQDSKDSYSL 180

QY 200 SSTLTSLKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 238

DB 181 SSTLTSLKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 219

RESULT 15

S37484

Ig kappa chain - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000

C;Accession: S37484

R;Ducancel, F.F.D.

submitted to the EMBL Data Library, February 1993

A;Reference number: S37483

A;Accession: S37484

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-225 <DUC>

A;Cross-references: EMBL:X70424; NID:g406254; PIDN:CAA49869.1; PID:g406255

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

Query Match

Best Local Similarity 60.5%; Pred. No. 6.5e-39;

Matches 138; Conservative 31; Mismatches 54; Indels 5; Gaps 2;

QY 11 LLLWVPGSTGEIVLTQSPGTSLSPGERATLSCASQSDY-DGDSYNNYQOKPGOAPRL 70

DB 3 LLLCVSGAHGSIYMTQPKFELISAGDRVTITCKASQSVSND----VAVYQQRPGQSPKL 58

QY 71 LIYAASNLSEGIPIRFSGSGGTDFLTTHPVEEADAATYYCOQSNEDPRTFGQGTKEI 130

DB 59 LIYASSRYTGVPDRFTGSGGTDFLTTHPVEEADAATYYCOQSNEDPRTFGQGTKEI 117

QY 131 KRTVAAPSVFIPTPPDEQLKSGTASVYVCLLNFPYREKAVQKVDNALQSGNSQESVTEQ 190

DB 118 KRADAAPTIVSIFPPSSSEQLTSGGASVVCFLNFPYKIDINVKWKIDGSRQNGVLNSWTDQ 177

QY 191 DSKDSTYSLSSTLTSLKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 238

DB 178 DSKDSTYSLSSTLTSLKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 225

Search completed: April 24, 2002, 15:11:39

Job time: 197 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 15:13:47 ; Search time 29.21 Seconds
(without alignments)
298.741 Million cell updates/sec

Title: US-09-499-662-109

Perfect score: 1245

Sequence: 1 METDRIILLWLLWVPSTGT.....EVTHQGLSPVTKSFNRGEC 238

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	550	44.2	131	1	KV3L_MOUSE
2	548	44.0	106	1	KAC_HUMAN
3	528	42.4	132	1	KV3F_MOUSE
4	516	41.4	111	1	KV3M_MOUSE
5	514	41.3	111	1	KV3N_MOUSE
6	512	41.1	111	1	KV3O_MOUSE
7	509	40.9	111	1	KV3Q_MOUSE
8	506.5	40.7	129	1	KV3L_HUMAN
9	501	40.2	111	1	KV3L_MOUSE
10	493.5	39.6	129	1	KV3M_HUMAN
11	491.5	39.5	110	1	KV3P_MOUSE
12	459	36.9	128	1	KV3K_HUMAN
13	453	36.4	111	1	KV3R_MOUSE
14	449	36.1	111	1	KV3H_MOUSE
15	445	35.7	111	1	KV3J_MOUSE
16	445	35.7	111	1	KV3S_MOUSE
17	444	35.7	111	1	KV3K_MOUSE
18	442.5	35.5	129	1	KV3H_HUMAN
19	439	35.3	111	1	KV3T_MOUSE
20	434.5	34.9	109	1	KV3B_HUMAN
21	433.5	34.8	109	1	KV3D_HUMAN
22	431	34.6	134	1	KV4E_HUMAN
23	429.5	34.5	109	1	KV3E_HUMAN
24	427	34.3	115	1	KV3L_HUMAN
25	426	34.2	111	1	KV3U_MOUSE
26	423	34.0	111	1	KV3C_MOUSE
27	422	33.9	112	1	KV3D_MOUSE
28	421.5	33.9	133	1	KV2F_HUMAN
29	420	33.7	111	1	KV3A_MOUSE
30	415.5	33.4	133	1	KV4B_HUMAN
31	414	33.3	129	1	KV1W_HUMAN
32	412.5	33.1	109	1	KV3G_HUMAN
33	412.5	33.1	112	1	KV3B_MOUSE

Query Match

44.2% Score 550; DB 1; Length 131;

ALIGNMENTS

RESULT 1

KV3L_MOUSE 111 33.0 411 111 KV3D_MOUSE
ID KV3L_MOUSE STANDARD; PRT; 131 AA.
AC P01661;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION MOPC 63 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-35.
RX MEDLINE=78235887; PubMed=98179;
RA Burstein Y., Schechter I.
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes.";
RL Biochemistry 17:2392-2400(1978).
RN [2]
RP SEQUENCE OF 21-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences.";
RN [3]
RX Biochemistry 12:760-771(1973).
RP REVISIONS
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
DR PIR; A01935; KVM5M6.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V3.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 131
FT DOMAIN 21 43
FT DOMAIN 44 58
FT DOMAIN 59 73
FT DOMAIN 74 80
FT DOMAIN 81 112
FT DOMAIN 113 121
FT DOMAIN 122 131
FT DISULFID 43 112
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;

34 411 33.0 111 KV3D_MOUSE
35 408 32.8 108 KV3V_MOUSE
36 401.5 32.2 108 KV3A_HUMAN
37 401.5 32.2 116 KV3J_HUMAN
38 397 31.9 114 KV4A_HUMAN
39 392.5 31.5 109 KV3F_HUMAN
40 388 31.2 108 KV1K_HUMAN
41 383 30.8 108 KV1M_HUMAN
42 383 30.8 108 KV5P_MOUSE
43 381.5 30.6 117 KV2E_HUMAN
44 381 30.6 108 KV1H_HUMAN
45 380 30.5 111 KV3E_MOUSE

P03977 mus musculus
P01674 mus musculus
P01619 homo sapien
P04434 homo sapien
P01625 homo sapien
P01624 homo sapien
P01605 homo sapien
P01649 mus musculus
P06309 homo sapien
P01600 homo sapien
P01657 mus musculus

```
Best Local Similarity 78.6%; Pred. No. 5.1e-38;
Matches 103; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

OY 1 METDTILLWLLVLPVPGSTGEIVLTQSPCTLSLSPGERATLSCAKASQSVVDYDGDSYMNNY 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 METDTILLWLLVLPVPGSTGNVLTQSPASLAISLGQRATISCRASESDVSYGNFIMHWY 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
OY 61 QOKPGQAPRLTIYAASNLSEIGIPDFSGSGGTDFTLTHPVEEDDAATYYCQSQNEDPR 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 QOKPGQPKLLIYLASNLSEIGVPAFSGSGSTDFTLIDPVEADDAATYYCQSQNEDPW 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
OY 121 TFGGQTKLEIK 131
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 121 TFGGQTKLEIK 131
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 2
KAC_HUMAN
ID KAC_HUMAN STANDARD; PRT; 106 AA.
AC P01834;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE IG KAPPA CHAIN C REGION.
GN IGKC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (MYELOMA PROTEIN EU).
RX MEDLINE=71064023; PubMed=5489770;
RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RL acid sequence of the light chain.";
RL Biochemistry 9:3155-3161(1970).
[2]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RL Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
[3]
RP SEQUENCE (BENCE-JONES PROTEIN TI).
RX MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RL immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
TI). IV. The complete amino acid sequence and its significance for
RL the mechanism of antibody production.";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE=81042304; PubMed=6775818;
RA Hietter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;
RT "Cloned human and mouse kappa immunoglobulin constant and J region
RL genes conserve homology in functional segments.";
RL Cell 22:197-207(1980).
[5]
RP SEQUENCE (BENCE-JONES PROTEIN ROY).
RX Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA Steinmetz-Kayne M., Suter L., Watanabe S.;
RL (In) Franek F., Sugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press,
RL New York (1969).
[6]
RP SEQUENCE (BENCE-JONES PROTEIN CUM).
RX MEDLINE=68242259; PubMed=5586923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
RL type).";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
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[7]
RN SEQUENCE (BENCE-JONES PROTEIN AG).
RP MEDLINE=69234734; PubMed=4693682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RL complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969).
[8]
RN SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
RP MEDLINE=70201507; PubMed=547531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RL chains.";
RL Science 169:56-59(1970).
CC -1- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
CC MARKER, 45-ALA AND 83-LEU.
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CC
CC EMBL: J00241; AAA58989.1;
CC EMBL: V00557; CAA23823.1;
CC PIR: A02116; K3HU.
CC MIM: 147200;
CC InterPro: IPR003006; Ig_MHC;
CC InterPro: IPR003597; Ig_C;
CC Pfam: PF00047; Ig; 1.
CC SMART: SM00407; IGCL; 1.
CC PROSITE: PS00290; IG_MHC;
CC Immunoglobulin domain; Immunoglobulin C region.
KW NON_TER
FT 1
FT DISULFID 26 86
FT DISULFID 106 106
FT VARIANT 83 83
FT
FT CONFLICT 14 14
FT CONFLICT 57 57
FT SEQUENCE 106 AA; 11609 MW; 51984D1FDD372CE8 CRC64;
SQ
Query Match 44.0%; Score 548; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 5.7e-38;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 133 TVAAPSVFIFFPPSDEQLKSGTNSVYVCLLNNEYPPEAKVQWKVDNALQSGNSQESVTEQDS 192
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 TVAAPSVFIFFPPSDEQLKSGTNSVYVCLLNNEYPPEAKVQWKVDNALQSGNSQESVTEQDS 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
OY 193 KDSYISLSSTLTLSKADYERKRVACEVTHOGLSSPVTKSFNRGEC 238
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 KDSYISLSSTLTLSKADYERKRVACEVTHOGLSSPVTKSFNRGEC 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
KV3F_MOUSE
ID KV3F_MOUSE STANDARD; PRT; 132 AA.
AC P01658;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION MOPC 321 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-37.
```

```
RX MEDLINE=78235887; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes.";
RL Biochemistry 17:2392-2400(1978).
RN [2]
RP SEQUENCE OF 21-132.
RX MEDLINE=73140224; PubMed=4120629;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Partial amino acid sequence of a kappa
RT chain.";
RL Biochemistry 12:749-759(1973).
CC -!- MISCELLANEOUS: THE PARTIAL SEQUENCE OF THE C REGION OF THIS
CC BENCE-JONES PROTEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT
CC REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY
CC RESIDUES.
CC PIR; A01933; KVM532.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW Immunoglobulin v region; Bence-Jones protein; Signal.
FT SIGNAL 1 20
FT CHAIN 21 132 IG KAPPA CHAIN V-III REGION MOPC 321.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 59 73 FRAMEWORK 2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 81 112 FRAMEWORK 3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 122 131 FRAMEWORK 4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON_TER 132 132
SQ SEQUENCE 132 AA; 14523 MW; 9F3B809BB773FBE9 CRC64;

Query Match 42.4%; Score 528; DB 1; Length 132;
Best Local Similarity 69.7%; Pred. No. 3.1e-36;
Matches 92; Conservative 26; Mismatches 14; Indels 0; Gaps 0;

QY 1 METDTLLWVLLWVPGSTGEIVLTQSPGTLSPGERATLSCASQSDVDYDGDSDYNNWY 60
DB 1 METDTLLWVLLWVPGSTGIVLTQSPASLAVSLGQRATISCKASQSDVDYDGDSDYNNWY 60

QY 61 QKPGQAPRLIIYAASNLGSDIPRFGSGSGTDFTLTTHPVEEDAAITYCQOSNEDPR 120
DB 61 ZKPGZPPKLLIYRASNLZSGIPARFSGSGRTBFTLTTPVZABDVATYFCZSZBZBPW 120

QY 121 TFGGQTKLEIKR 132
DB 121 TFGSGTKLEIKR 132

RESULT 4
KV3M_MOUSE STANDARD; PRT; 111 AA.
AC P01665;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7043.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; B01937; KVM583.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW Immunoglobulin v region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Query Match 41.3%; Score 514; DB 1; Length 111;
Best Local Similarity 86.5%; Pred. No. 3.4e-35;
Matches 96; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
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RL Nature 276:785-790(1978).
DR PIR; A01937; KVM543.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW Immunoglobulin v region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 41.4%; Score 516; DB 1; Length 111;
Best Local Similarity 87.4%; Pred. No. 2.3e-35;
Matches 97; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 21 EIVLTQSPGTLSPGERATLSCASQSDVDYDGDSDYNNWYQKPGQAPRLIIYAASNL 80
DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDYDGDSDYNNWYQKPGQAPRLIIYAASNL 60

QY 81 GIPDRFGSGSGTDFTLTTHPVEEDAAITYCQOSNEDPRFTGGQTKLEIK 131
DB 61 GIPARFSGSGSGTDFTLTTHPVEEDAAITYCQOSNEDPRFTFGSGTKLEIK 111

RESULT 5
KV3N_MOUSE STANDARD; PRT; 111 AA.
ID KV3N_MOUSE STANDARD; PRT; 111 AA.
AC P01666;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7183.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; B01937; KVM583.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW Immunoglobulin v region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Query Match 41.3%; Score 514; DB 1; Length 111;
Best Local Similarity 86.5%; Pred. No. 3.4e-35;
Matches 96; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
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[illegible]

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FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; D3C55292772774D0 CRC64;

Query Match
Best Local Similarity 40.78; Score 506.5; DB 1; Length 129;
Matches 100; Conservative 10; Mismatches 19; Indels 3; Gaps 1;

QY 1 METDTILLWLLVMPGSGTGLVTSQPTLSLSPGERATLSCKASQSDVDGDSYNNWY 60
DB 1 METPAQLFLLLWLPDPTGTVLTSQPTLSLSPGERATLSCKASQSV---SSSYLAWY 57

QY 61 QKQKQAPRLIYAASNLGIPDRFGSGSGTDFTLTIHPVEEDAATYYCQSNEDPR 120
DB 58 QKQKQAPRLIYGASSRATGIPDRFGSGSGTDFTLTIISRLPEDFAVYCYQYGTSPR 117

QY 121 TFGQGTKEIKR 132
DB 118 TFGQGTKEIKR 129

RESULT 9
KV3L_MOUSE
ID KV3L_MOUSE STANDARD; PRT; 111 AA.
AC P01664;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION CBPC 101.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3917-3917 (1978).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01936; KVMSC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; E2BIAD98AD965962 CRC64;

Query Match
Best Local Similarity 40.28; Score 501; DB 1; Length 111;
Matches 94; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 21 EIVLTQSPGTLSPGERATLSCKASQSDVDGDSYNNWYQKQKQAPRLIYAASNLG 80
DB 1 DIVLTQSPASLAVSLGQRATLSCKASQSDVDYTGSEYNNWYQNFQSPKLLIYAASNLG 60

QY 81 GIPDRFGSGSGTDFTLTIHPVEEDAATYYCQSNEDPRTFGQGTKEIK 131
DB 61 GIPARFGSGSGTDFTLNIHPVEEDAATYYCQSNEDPYTFGGGTKEIK 111
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RESULT 10
KV3M_HUMAN
ID KV3M_HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION HIC PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR; P10021; K3HUHI.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 20
FT DOMAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 7395528EA2BB74D6 CRC64;

Query Match
Best Local Similarity 39.68; Score 493.5; DB 1; Length 129;
Matches 98; Conservative 10; Mismatches 21; Indels 3; Gaps 1;

QY 1 METDTILLWLLVMPGSGTGLVTSQPTLSLSPGERATLSCKASQSDVDGDSYNNWY 60
DB 1 METPAQLFLLLWLPDPTGTVLTSQPTLSLSPGERATLSCKASQSV---SSSYLAWY 57

QY 61 QKQKQAPRLIYAASNLGIPDRFGSGSGTDFTLTIHPVEEDAATYYCQSNEDPR 120
DB 58 QKQKQAPRLIYGASSRATGIPDRFGSGSGTDFTLTIISRLPEDFAVYCYQYGTSPW 117

QY 121 TFGQGTKEIKR 132
DB 118 TFGQGTKEIKR 129

RESULT 11
KV3P_MOUSE
ID KV3P_MOUSE STANDARD; PRT; 110 AA.
AC P01668;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7210.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR; D01937; KVM510.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 100
FT DOMAIN 101 110
FT DISULFID 23 92
FT NON_TER 110 110
SQ SEQUENCE 110 AA; 11950 MW; 69F1A5CE886B1249 CRC64;

Query Match 39.5%; Score 491.5; DB 1; Length 110;
Best Local Similarity 84.7%; Pred. No. 2.2e-33;
Matches 94; Conservative 8; Mismatches 38; Indels 1; Gaps 1;

OY 21 EIVLTQSPGTLSPGERATLSCAKASQVDYDGDSDYMNWYQKPGQAPRLIIYAASNL 80
DB 1 DIVLTQSPASLAVSGQRATISCKASQSLDYGSDYMNWYQKPGQPKLLIIYAASNL 60
OY 81 GIPDRFSGSGGTDFLTTHPVEEDAATYYCQQSNEDPRTFGQGTGLEIK 131
DB 61 GIPARFSGSGGTDFLTTHPVEEDAATYYCHQS-EDPWTFGSGTGLEIK 110

RESULT 12
KV3K_HUMAN
ID KV3K_HUMAN STANDARD; PRT; 128 AA.
AC P06311;
DT 01-JAN-1988 (Rel. 05, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION IARC/BL41 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
III.";
RL Nucleic Acids Res. 13:6499-6513(1985).
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DR EMBL; Z00021; CAA77316.1; -.
DR PIR; A01899; K3HU41.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
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DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 128
FT DOMAIN 21 43
FT DOMAIN 44 54
FT DOMAIN 55 69
FT DOMAIN 70 76
FT DOMAIN 77 108
FT DOMAIN 109 117
FT DOMAIN 118 128
FT DISULFID 43 108
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;

Query Match 36.9%; Score 459; DB 1; Length 128;
Best Local Similarity 71.2%; Pred. No. 1.2e-30;
Matches 94; Conservative 11; Mismatches 23; Indels 4; Gaps 1;

OY 1 METDTILLWVLLWVPGSTGEIVLTQSPCTLSLSPGERATLSCAKASQVDYDGDSDYMNWY 60
DB 1 METPAQLFLLLWLPDPTGEIVLTQSPCTLSLSPGERATLSCAKASQV----SSNLAWY 56
OY 61 QOKPGQAPRLIIYAASNLSEGPDRFSGSGGTDFLTTHPVEEDAATYYCQQSNEDPR 120
DB 57 QOKRQSPRLIIRDASSRANGIPDRFSGSGGTDFLTILSRLEPEDFAVYYCQYSTSPY 116
OY 121 TFGQGTGLEIKR 132
DB 117 TFGQGTGLEIKR 128

RESULT 13
KV3R_MOUSE
ID KV3R_MOUSE STANDARD; PRT; 111 AA.
AC P01670;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 6684.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR; A01938; KVM584.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12039 MW; 1E46988341858526 CRC64;

Query Match 36.4%; Score 453; DB 1; Length 111;
Best Local Similarity 77.5%; Pred. No. 2.9e-30;
Matches 86; Conservative 11; Mismatches 14; Indels 0; Gaps 0;
```

```
Oy 21 EIVLTQSPGTLSPGERATISCKASQSDYDGDSDYNNWYQKQPGAPRLIIYAASNLES 80
      :||||| :|:| :|:|:|:|:|:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1 DIVLTQSPASLAVSLGQRATISCRASKSVSTGYSYHMYQKQPGQPKLLIYASNLES 60

Oy 81 GIPDRFSGSGGTDFLTTHIHPVEEDAATYCCQSNEDPRTFGGQTKLEIK 131
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 61 GVPARFSGSGGTDFLTTHIHPVEEDAATYCCQHSRELPRTFGGGQTKLEIK 111

RESULT 15
KV3H_MOUSE
ID KV3H_MOUSE STANDARD; PRT; 111 AA.
AC P01660;
DT 21-JUL-1986 (Rel. 01, Created)
DE 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 3741/TEPC 111.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (PC 3741).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
RN [2]
RP SEQUENCE (TEPC 111).
RX MEDLINE=79073152; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -!- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
DR PIR; A01934; KVM537.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT FT DOMAIN 24 38
FT FT DOMAIN 39 53
FT FT DOMAIN 54 60
FT FT DOMAIN 61 92
FT FT DOMAIN 93 101
FT FT DOMAIN 102 111
FT FT DISULFID 23 92
FT FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;

Query Match 36.1%; Score 449; DB 1; Length 111;
Best Local Similarity 76.6%; Pred. No. 6.2e-30;
Matches 85; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

Oy 21 EIVLTQSPGTLSPGERATISCKASQSDYDGDSDYNNWYQKQPGAPRLIIYAASNLES 80
      :||||| :|:| :|:|:|:|:|:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1 DIVLTQSPASLAVSLGQRATISCRASESDYSGNSFHHYQKQPGQPKLLIYASNLES 60

Oy 81 GIPDRFSGSGGTDFLTTHIHPVEEDAATYCCQSNEDPRTFGGQTKLEIK 131
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 61 GIPARFSGSGGTDFLTTHIHPVEADDAATYCCQSNEDPRTFGGQTKLEIK 111

RESULT 15
KV3J_MOUSE
ID KV3J_MOUSE STANDARD; PRT; 111 AA.
AC P01662;
DT 21-JUL-1986 (Rel. 01, Created)
```

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DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION ABPC 22/PC 9245.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (ABPC 22).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
RN [2]
RP SEQUENCE (PC 9245).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
CC -!- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
DR PIR; A01935; KVM56.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT FT DOMAIN 24 38
FT FT DOMAIN 39 53
FT FT DOMAIN 54 60
FT FT DOMAIN 61 92
FT FT DOMAIN 93 101
FT FT DOMAIN 102 111
FT FT DISULFID 23 92
FT FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;

Query Match 35.7%; Score 445; DB 1; Length 111;
Best Local Similarity 76.4%; Pred. No. 1.3e-29;
Matches 84; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

Oy 22 IVLTQSPGTLSPGERATISCKASQSDYDGDSDYNNWYQKQPGAPRLIIYAASNLES 81
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 2 IVLTQSPASLAVSLGQRATISCRASESDYSGNSFHHYQKQPGQPKLLIYASNLES 61

Oy 82 IPDRFSGSGGTDFLTTHIHPVEEDAATYCCQSNEDPRTFGGQTKLEIK 131
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 62 VPARFSGSGGTDFLTTHIHPVEADDAATYCCQNNEDPRTFGGQTKLEIK 111
```

Search completed: April 24, 2002, 15:13:47
Job time: 324 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 15:13:12 ; Search time 86.76 Seconds
(without alignments)
401.254 Million cell updates/sec

Title: US-09-499-662-109

Perfect score: 1245

Sequence: 1 METDTILLVLLWVPGSTG.....EVTHQGLSSPVTKSFNRGEC 238

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	743.5	59.7	238	11	Q99M37	Q99M37 mus musculus
2	679	54.5	214	11	Q9RIA5	Q9RIA5 mus musculus
3	433.5	34.8	235	11	Q99M11	Q99M11 mus musculus
4	432.5	34.7	109	4	Q9UL78	Q9UL78 homo sapien
5	399.5	32.1	109	4	Q9UL86	Q9UL86 homo sapien
6	394	31.6	103	11	Q9JL80	Q9JL80 mus musculus
7	391	31.4	108	4	Q9UL77	Q9UL77 homo sapien
8	387	31.1	108	4	Q9UL83	Q9UL83 homo sapien
9	384	30.8	108	4	Q9UL79	Q9UL79 homo sapien
10	382	30.7	108	4	Q9UL70	Q9UL70 homo sapien
11	378.5	30.4	109	4	Q9UL85	Q9UL85 homo sapien
12	369.5	29.7	107	4	Q9UL81	Q9UL81 homo sapien
13	355	28.5	114	4	Q9UL80	Q9UL80 homo sapien
14	354.5	28.5	106	5	Q9U410	Q9U410 schistosoma
15	338	27.1	107	11	Q9ER29	Q9ER29 mus musculus
16	332	26.7	99	11	Q9JL74	Q9JL74 mus musculus
17	331	26.6	101	11	Q9JL78	Q9JL78 mus musculus
18	330	26.5	97	11	Q9JL76	Q9JL76 mus musculus
19	324.5	26.1	104	11	Q9JL82	Q9JL82 mus musculus

20	320	25.7	298	11	Q9QYF0	Q9QYF0 mus musculus
21	297	23.9	107	11	Q9JL84	Q9JL84 mus musculus
22	288	23.1	109	6	Q9N0W5	Q9N0W5 oryctolagus
23	249	20.0	107	4	Q9UL82	Q9UL82 homo sapien
24	237.5	19.1	107	4	Q9NSD6	Q9NSD6 homo sapien
25	228	18.3	130	11	Q9DBW4	Q9DBW4 mus musculus
26	225	18.1	130	4	Q9NP29	Q9NP29 homo sapien
27	203	16.3	484	11	Q99JLA6	Q99JLA6 mus musculus
28	201	16.1	267	13	Q90529	Q90529 ginglymosto
29	197.5	15.9	463	10	Q99JLC4	Q99JLC4 mus musculus
30	197	15.8	473	10	Q9DBL4	Q9DBL4 mus musculus
31	189.5	15.2	509	10	Q90907	Q90907 mus musculus
32	189.5	15.2	509	10	Q90X57	Q90X57 mus musculus
33	189.5	15.2	513	10	P97797	P97797 mus musculus
34	183	14.7	361	4	Q9H1U5	Q9H1U5 homo sapien
35	181.5	14.6	468	11	Q99JL31	Q99JL31 mus musculus
36	180.5	14.5	268	10	Q90524	Q90524 ginglymosto
37	180.5	14.5	479	10	Q99M22	Q99M22 mus musculus
38	178.5	14.3	506	6	O46631	O46631 bos taurus
39	178.5	14.3	509	11	Q9WTN4	Q9WTN4 mus musculus
40	178	14.3	398	4	O00241	O00241 homo sapien
41	176	14.1	372	4	Q9Y4V0	Q9Y4V0 homo sapien
42	175.5	14.1	509	11	P97710	P97710 rattus norv
43	175	14.1	473	11	Q99JL25	Q99JL25 mus musculus
44	174	14.0	105	11	Q99JJC1	Q99JJC1 mus musculus
45	173.5	13.9	509	11	Q9QW15	Q9QW15 rattus norv

ALIGNMENTS

RESULT 1	
Q99M37	
ID Q99M37	PRELIMINARY; PRT; 238 AA.
AC Q99M37	
DT 01-JUN-2001 (TrEMBLrel. 17, Created)	
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)	
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)	
DE UNKNOWN (PROTEIN FOR MGC:5947).	
OS Mus musculus (Mouse).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX NCBI_TaxID=10090;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC TISSUE=MAMMARY TUMOR;	
RA Strausberg R.;	
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.	
DR EMBL; BC002035; AAH02035.1; -	
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B0801330A CRC64;	

Query Match	59.7%	Score 743.5;	DB 11;	Length 238;
Best Local Similarity	58.5%	Pred. No. 3.2e-61;		
Matches 137;	Conservative 441;	Mismatches 55;	Indels 1;	Gaps 1;
QY 6	ILLVLLVLPVPGSTGEIVLFG	PGCTLSLSPGERATLSCAKASQSDYD	-DGDSYMNYQOKP	64
Db 5	VRLVLFWIPASSDSDVMTG	TPLSLVSLGDAQISCRSSQSVHSNGNTL	EYLYLQKP	64
QY 65	GOAPRLIYAASNLGSGIDP	FGSGSGTDTFTLTHPVEEEDAATY	YCCQSNEDPRTFGQ	124
Db 65	GQSPKLLIYKSVNRFSGVP	DRFGSGSGTDTFTLKISRVEAEDL	GVYCFQGSHPYTFGS	124
QY 125	GTKLEIKRTVAASVFIFPP	SDGOLKSGTASVVCLLNNFP	PREAKVQKWVNAQNSQ	184
Db 125	GTKLEIKRADAAPTSTVF	PPSPSEQLTSGGASVVCFLNN	FYPKOINVKWKGDSERQNGVL	184
QY 185	ESVTEODSKDSTVSLSTL	TLSKADYEKKVYACEVTHQGL	SSPVTKSFNRGEC	238
Db 185	NSWTDQDQSKDSTVSMST	LTLTDKDEYERHNSYCEATH	TKTSTSPIVAKSFNRNEC	238

SQ SEQUENCE 235 AA; 25403 MW; 39807BFE6782A3FB CRC64;
 Query Match 34.88; Score 432.5; DB 11; Length 235;
 Best Local Similarity 43.08; Pred. No. 1.9e-32;
 Matches 102; Conservative 36; Mismatches 86; Indels 13; Gaps
 Qy 7 LLWVLLWVPGSTGEIVLTQSPGTLSPGERATLSCKASQSDYDGDGSYNNYQQKPGQ 66
 Db 6 LLLVFLHLLTGSCAQLVLTQ--PSSVSTSLGSTAKLPCKA--STGNIGDSYNNYQQYVNGR 62
 Qy 67 APRLLIYAASNLGSGIDPRSGS--GSGTDFTLTIHPVEEEDAAITYCQGSNEDPRTFQG 124
 Db 63 SPTNNIYGDDLRPSGVSDFRSGSDSSNSGAFTIQNWQADDEADYYCQSYSSGIRVFGG 122
 Qy 125 GTKLEI-KRTVAAPSVFFPPSDBLKSGTASVVCVLLNNEYPREAKVQWVDNALSGNS 183
 Db 123 GTKLTVLSQPKTSPSVLTFPPSSSELENTKATLVCTISDFYPGVVVDWADG---TPVT 179
 Qy 184 QESVTEQDSK--DSYSLSELTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 238
 Db 180 QGVETTPQSKNNKYMASVLTLTAKAWETHSSYSCOVTHEG--HTVEKSLRADC 234
 RESULT 4
 ID Q9UL78 PRELIMINARY; PRT; 109 AA.
 AC Q9UL78;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT)
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RU Wu X., Liu B., Van der Meewe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 CC -1 SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR ENBL; AF035036; AAD56272.1; -
 DR HSP; P01789; IACP.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 109
 SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;
 Query Match 34.78; Score 432.5; DB 4; Length 109;
 Best Local Similarity 76.88; Pred. No. 8.8e-33;
 Matches 86; Conservative 6; Mismatches 17; Indels 3; Gaps
 Qy 21 EIVLTQSPGTLSPGERATLSCKASQSDYDGDGSYNNYQQKPGQAPRLIYAASNLDS 80
 Db 1 EIVLTQSPGTLSPGERATLSCRASQSV---SSSLAWYQQKPGQAPRLIYGASSRAT 57
 Qy 81 GIDPRFSGSGSGTDFTLTIHPVEEEDAAITYCQGSNEDPRTEGQTKLEIKR 132
 Db 58 GIDPRFSGSGSGTDFTLTISSLRLEPEDCAVYVYQQYVGGSSPLTFGGGTTKVEIKR 109
 RESULT 5
 ID Q9UL86 PRELIMINARY; PRT; 109 AA.
 AC Q9UL86;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT)
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RU Wu X., Liu B., Van der Meewe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 CC -1 SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR ENBL; AF035036; AAD56272.1; -
 DR HSP; P01789; IACP.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 109
 SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Q9UL86;
 01-MAY-2000 (TREMBlrel. 13, Created)
 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 DOMAIN.
 DR EMBL; AF035028; AAD56264.1; -.
 DR HSSP; P01789; IMCP.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;
 SQ

Query Match 32.1%; Score 399.5; DB 4; Length 109;
 Best Local Similarity 72.3%; Pred. No. 1e-29;
 Matches 81; Conservative 7; Mismatches 21; Indels 3; Gaps 1;

QY 21 EIVLTQSPGCTLSLSPGERATLSCASQSVYDGDYSYMWYQKPGQAPRLIIYAASNLES 80
 Db 1 EIVLTQSPGCTLSLSPGERATLSCASQSVYDGDYSYMWYQKPGQAPRLIIYAASNLES 57
 [1]
 QY 81 GPIPRFSGSGSTDTFTLTHPVEEDAAITYCQSNEDPRTFGQTKLEIKR 132
 [1]
 Db 58 GPIPRFSGSGSTDTFTLTHPVEEDAAITYCQSNEDPRTFGQTKLEIKR 109
 [1]
 RESULT 6
 Q9JL80 PRELIMINARY; PRT; 103 AA.
 ID Q9JL80;
 AC Q9JL80;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
 acetyl-glucosamine antibodies from mice with autoimmune myocarditis";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 DOMAIN.
 DR EMBL; AF206026; AAF69324.1; -.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 103
 FT SEQUENCE 103 AA; 11224 MW; EC87D653DB3AAB21 CRC64;
 SQ

Query Match 31.63%; Score 394; DB 11; Length 103;
 Best Local Similarity 71.63%; Pred. No. 3.1e-29;
 Matches 73; Conservative 15; Mismatches 14; Indels 0; Gaps 0;

QY 30 TISLSPGERATLSCASQSVYDGDYSYMWYQKPGQAPRLIIYAASNLESIGIPDRFSGS 89
 Db 2 SLAVSLGQRATISCRASESVKGTSLMOWYQKPGQAPRLIIYAASNLESIGIPDRFSGS 61
 [1]
 QY 90 GSGTDTFTLTHPVEEDAAITYCQSNEDPRTFGQTKLEIKR 131
 [1]
 Db 62 GSGTDTFTLTHPVEEDAAITYCQSNEDPRTFGQTKLEIKR 103
 [1]
 RESULT 7
 Q9UL77 PRELIMINARY; PRT; 108 AA.
 ID Q9UL77;
 AC Q9UL77;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 DOMAIN.
 DR EMBL; AF035037; AAD56273.1; -.
 DR HSSP; P01607; IREI.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 108
 FT SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;
 SQ

Query Match 31.43%; Score 391; DB 4; Length 108;
 Best Local Similarity 66.13%; Pred. No. 6.2e-29;
 Matches 74; Conservative 17; Mismatches 17; Indels 4; Gaps 1;

QY 21 EIVLTQSPGCTLSLSPGERATLSCASQSVYDGDYSYMWYQKPGQAPRLIIYAASNLES 80
 Db 1 DIOMTQSPSLSASVGDRTVTECRASQSI-----SSLYNMYQKPGKAPNLLIIYAASLQS 56
 [1]
 QY 81 GPIPRFSGSGSTDTFTLTHPVEEDAAITYCQSNEDPRTFGQTKLEIKR 132
 [1]
 Db 57 GVPFRSGSGSGTDTFTLTHPVEEDAAITYCQSNEDPRTFGQTKLEIKR 108
 [1]
 RESULT 8
 Q9UL83 PRELIMINARY; PRT; 108 AA.
 ID Q9UL83;
 AC Q9UL83;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN NCBI_TaxID=9606;
 [1]

```

RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -/- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035031; AAD56267.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
DR NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 31.1%; Score 387; DB 4; Length 108;
Best Local Similarity 69.6%; Pred. No. 1.5e-28;
Matches 78; Conservative 10; Mismatches 20; Indels 4; Gaps 1;

QY 21 EIVLTQSPGTLSPGERATLSCAKSQSYVDYDGSYMMYQKPGQAPRLIYAASNL80
Db 1 EIVMTQSPATLSVSPGERATLSCRSQSV----SSNLAWYQKPGQAPRLIYCASTRAT 56

QY 81 GIPDRFSGSGGTDFTLTHPVEEEDATYYCOQSNEDPRTFGQGTKEIKR 132
Db 57 GIPARFSGSGGTDFTLTHPVEEEDATYYCOQSNEDPRTFGQGTKEIKR 108

RESULT 9
Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -/- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035044; AAD56280.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
DR NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 30.7%; Score 382; DB 4; Length 108;
Best Local Similarity 63.4%; Pred. No. 4.2e-28;
Matches 71; Conservative 17; Mismatches 20; Indels 4; Gaps 1;

QY 21 EIVLTQSPGTLSPGERATLSCAKSQSYVDYDGSYMMYQKPGQAPRLIYAASNL80
Db 1 DIQMTQSPSSLASVGDRTVTFCRASQGI----SNFLAWYQKPGKVPKSLIYAASLTQ5 56

QY 81 GIPDRFSGSGGTDFTLTHPVEEEDATYYCOQSNEDPRTFGQGTKEIKR 132
Db 57 GVPFRSGSGGTDFTLTHPVEEEDATYYCOQSNEDPRTFGQGTKEIKR 108

RESULT 11
Q9UL85 PRELIMINARY; PRT; 109 AA.
AC Q9UL85;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -/- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035035; AAD56271.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
DR NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 30.8%; Score 384; DB 4; Length 108;
Best Local Similarity 66.1%; Pred. No. 2.8e-28;
Matches 74; Conservative 13; Mismatches 21; Indels 4; Gaps 1;

QY 21 EIVLTQSPGTLSPGERATLSCAKSQSYVDYDGSYMMYQKPGQAPRLIYAASNL80
Db 1 DIVMTQSPSLASVGDRTVTFCSRMSQGI----SSNLAWYQKPGKAPPELLIYAASLTQ5 56

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QY 81 GIPDRFSGSGGTDFTLTHPVEEEDATYYCOQSNEDPRTFGQGTKEIKR 132
Db 57 GVPFRSGSGGTDFTLTHPVEEEDATYYCOQSNEDPRTFGQGTKEIKR 108

RESULT 10
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -/- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035044; AAD56280.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
DR NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 30.7%; Score 382; DB 4; Length 108;
Best Local Similarity 63.4%; Pred. No. 4.2e-28;
Matches 71; Conservative 17; Mismatches 20; Indels 4; Gaps 1;

QY 21 EIVLTQSPGTLSPGERATLSCAKSQSYVDYDGSYMMYQKPGQAPRLIYAASNL80
Db 1 DIQMTQSPSSLASVGDRTVTFCRASQGI----SNFLAWYQKPGKVPKSLIYAASLTQ5 56

QY 81 GIPDRFSGSGGTDFTLTHPVEEEDATYYCOQSNEDPRTFGQGTKEIKR 132
Db 57 GVPFRSGSGGTDFTLTHPVEEEDATYYCOQSNEDPRTFGQGTKEIKR 108

RESULT 11
Q9UL85 PRELIMINARY; PRT; 109 AA.
AC Q9UL85;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -/- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.

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CC      DOMAIN.
DR      EMBL; AF035029; AAD56265.1; -.
DR      HSSP; P01607; 1REI.
DR      InterPro; IPR003006; Ig_MHC.
DR      Pfam; PF00047; Ig; 1.
DR      SMART; SM00406; IGV; 1.
FT      NON_TER 109 109
FT      SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFAACC CRC64;

Query Match      30.4%; Score 378.5; DB 4; Length 109;
Best Local Similarity 69.0%; Pred. No. 9.1e-28;
Matches 78; Conservative 10; Mismatches 20; Indels 5; Gaps 2;

QY      21 EIVLTQSPGTLSPGERATFLSCASQSDYDGDGYNNYQKPGQAPRLLIYAASNL 80
DB      1 EIVWTQSPATLSVPERATFLSCWASQSI-----SSNLWTQQKPGQAPRLLIYGASTRAT 56

QY      81 GIPDRFSGSGSGDTFTLTTHPVEEADAATVYCOQSNE-DPRTFCQGTKLEIKR 132
DB      57 GIPARFSGSGSGTEFTLTITSLQSEDAFIVHCQYNSWPLTFTGGTKVEIKR 109

RESULT 12
Q9UL81      PRELIMINARY; PRT; 107 AA.
AC      Q9UL81;
DT      01-MAY-2000 (TrEMBLrel. 13, Created)
DT      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT      01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE      MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98277139; PubMed=9614934;
RA      Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA      Young D.C.;
RT      "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT      fetus.";
RL      Clin. Immunol. Immunopathol. 87:184-192(1998).
CC      -|- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC      DOMAIN.
DR      EMBL; AF035033; AAD56269.1; -.
DR      HSSP; P80362; 1WTL.
DR      InterPro; IPR003006; Ig_MHC.
DR      Pfam; PF00047; Ig; 1.
DR      SMART; SM00406; IGV; 1.
FT      NON_TER 107 107
FT      SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match      29.7%; Score 369.5; DB 4; Length 107;
Best Local Similarity 63.4%; Pred. No. 6.1e-27;
Matches 71; Conservative 19; Mismatches 17; Indels 5; Gaps 2;

QY      21 EIVLTQSPGTLSPGERATFLSCASQSDYDGDGYNNYQKPGQAPRLLIYAASNL 80
DB      1 DIQWTQSPSLASVGDRTVITCRASQSI-----SNLNTWQQKPGKAPNLLIYAASLQS 56

QY      81 GIPDRFSGSGSGDTFTLTTHPVEEADAATVYCOQSNE-DPRTFCQGTKLEIKR 132
DB      57 GVPFRFSGSGSGDTFTLTISGLQAEAFATVYCOQS-YSAITFGPGKVDIR 107

RESULT 13
Q9UL80      PRELIMINARY; PRT; 114 AA.
AC      Q9UL80;
DT      01-MAY-2000 (TrEMBLrel. 13, Created)
DT      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT      01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE      MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98277139; PubMed=9614934;
RA      Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA      Young D.C.;
RT      "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT      fetus.";
RL      Clin. Immunol. Immunopathol. 87:184-192(1998).
CC      -|- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC      DOMAIN.
DR      EMBL; AF035034; AAD56270.1; -.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; Ig; 1.
DR      SMART; SM00406; IGV; 1.
FT      NON_TER 114 114
FT      SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match      28.5%; Score 355; DB 4; Length 114;
Best Local Similarity 59.6%; Pred. No. 1.5e-25;
Matches 68; Conservative 20; Mismatches 24; Indels 2; Gaps 2;

QY      21 EIVLTQSPGTLSPGERATFLSCASQSDYDGDGYNNYQKPGQAPRLLIYAASNL 79
DB      1 DVVWTQSPLSLPTLVTRQSPASISCRSSPSVSDGNTYLNWFQKPGQAPRLLIYKVSNRD 60

QY      80 SGIPDRFSGSGSGDTFTLTTHPVEEADAATVYCOQSNE-DPRTFCQGTKLEIKR 132
DB      61 SGVPDRFSGSGSGDTFTLTISRVEADGVYVYCMQGTHTWPTFGQTKVEIKR 114

RESULT 14
Q9U410      PRELIMINARY; PRT; 106 AA.
AC      Q9U410;
DT      01-MAY-2000 (TrEMBLrel. 13, Created)
DT      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT      01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE      MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
DE      VARIABLE REGION (FRAGMENT).
OS      Schistosoma japonicum (Blood fluke).
OC      Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC      Trematoda; Digenea; Strigeida; Schistosomatoidea; Schistosomatidae;
OC      Schistosoma.
OX      NCBI_TaxID=6182;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
RT      "Amplification, cloning and sequence analysis of the light chain
RT      variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT      Schistosoma japonicum.";
RL      Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC      -|- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC      DOMAIN.
DR      EMBL; AF207620; AAF19434.1; -.
DR      HSSP; P01679; 2FBJ.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; Ig; 1.
DR      SMART; SM00406; IGV; 1.
FT      NON_TER 111 111
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Job time: 290 sec

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FT NON_TER 106 106
SQ SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;

Query Match      28.5%; Score 354.5; DB 5; Length 106;
Best Local Similarity 63.1%; Pred. No. 1.5e-25;
Matches 70; Conservative 12; Mismatches 24; Indels 5; Gaps 1;

Qy 21 EIVLTQSPGTLISLSPGERATLSCAKSQSV--DYDGSYMMWYQKPGQAPRLLIYAASNL 80
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 ENLLTQSPAINASGKGVKVTCSASSV----SYVYVYLQKPGSSPRLLIYDTSNLAS 55

Qy 81 GIPDRFSGSGGTFTLTTHPVEEDAAATYYCQOSNEDPRTFGGQTKLEIK 131
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 56 GVPVRFSGSGGTFTLTISRMEADAATYYCQOWTSYPFTFGSGTKLELK 106

RESULT 15
Q9ERZ9 PRELIMINARY; PRT; 107 AA.
AC Q9ERZ9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;
RT "Cloning and sequencing of the light chain fragment of variable region
RL genes of an anti-hTNF-a monoclonal antibody.";
RN [2]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT "Construction and sequencing of the single-chain antibody gene of a
RL human TNF-alpha specific monoclonal antibody.";
RN [3]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
   DOMAIN.
DR EMBL: AF262753; AAC23804.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00409; IG; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11784 MW; 2B15EEA6604A26C3 CRC64;

Query Match      27.1%; Score 338; DB 11; Length 107;
Best Local Similarity 59.8%; Pred. No. 5.1e-24;
Matches 64; Conservative 16; Mismatches 25; Indels 2; Gaps 1;

Qy 24 LTQSPGTLISLSPGERATLSCAKSQSV--DYDGSYMMWYQKPGQAPRLLIYAASNL 81
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MTQSPSLAMSGKVTMCKSSQSVLSNTQKYNLAWYQKPGQSPPELLLYFASTRESG 60

Qy 82 IPDRFSGSGGTFTLTTHPVEEDAAATYYCQOSNEDPRTFGGQTKL 128
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 VPDFRMGSGGTFTLTISRMEADAATYYCQOWTSYPFTFGSGTKLEIK 107

Search completed: April 24, 2002, 15:13:12
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 15:08:17 ; Search time 85.18 Seconds
(without alignments)
206.967 Million cell updates/sec

Title: US-09-499-662-50

Perfect score: 1242

Sequence: 1 METDTILLWLLVLLPGSTG.....EVTHGLSSPVTKSFNRGEC 238

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 4: /SID58/gcgdata/geneseq/geneseq/AA1983.DAT.*
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- 21: /SID58/gcgdata/geneseq/geneseq/AA2000.DAT.*
- 22: /SID58/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1242	100.0	238	19 AAW83031	Anti-Fas humanised
2	1242	100.0	238	21 AAB14772	Humanised anti-Fas
3	1242	100.0	238	21 AAW90922	Humanised anti-Fas
4	1230	99.0	238	19 AAW83034	Anti-Fas humanised
5	1230	99.0	238	21 AAB14777	Humanised anti-Fas
6	1230	99.0	238	21 AAW90927	Humanised HFE7A de
7	1202	96.8	238	19 AAW83032	Anti-Fas humanised
8	1202	96.8	238	21 AAB14773	Humanised anti-Fas
9	1202	96.8	238	21 AAW90923	Humanised anti-Fas
10	1195	96.2	238	19 AAW83035	Anti-Fas humanised
11	1195	96.2	238	21 AAB14778	Humanised anti-Fas

12	1195	96.2	238	21	AAW90928	Humanised HFE7A de
13	1194	96.1	238	19	AAW83033	Anti-Fas humanised
14	1194	96.1	238	21	AAB14774	Humanised anti-Fas
15	1194	96.1	238	21	AAW90924	Humanised anti-Fas
16	1172	94.4	238	21	AAW90931	Humanised anti-Fas
17	1169	94.1	238	21	AAW90932	Humanised anti-Fas
18	1168	94.0	238	21	AAW90930	Humanised anti-Fas
19	1061.5	85.5	235	21	AAW93702	The kappa chain of
20	1061.5	85.5	235	21	AAW93729	The kappa chain of
21	1047	84.3	234	21	AAW93708	The kappa chain of
22	1047	84.3	234	21	AAW93733	The kappa chain of
23	1047	84.3	234	21	AAW92239	Human bone marrow
24	1045	84.1	218	18	AAW13363	Humanised anti-L-s
25	1044.5	84.1	233	21	AAW93704	The kappa chain of
26	1044.5	84.1	233	21	AAW93731	The kappa chain of
27	1033	83.2	240	20	AAW50161	Human reshaped F19
28	1031	83.0	218	20	AAW95658	Mus musculus anti-
29	1031	83.0	218	21	AAW85200	Light chain amino
30	1031	83.0	218	22	AAW76947	Full variable ligh
31	1026.5	82.6	384	22	AAU14461	Human novel protei
32	1026.5	82.6	384	22	AAU14462	Human novel protei
33	1026.5	82.6	384	22	AAU14463	Human novel protei
34	1026.5	82.6	384	22	AAU14464	Human novel protei
35	1024	82.4	218	14	AAW33312	Humanised MaEl1 Ve
36	1023	82.4	236	22	AAW71272	Human gene 2-encod
37	1012	81.5	237	20	AAW73873	Human anticirc epsi
38	1008	81.2	218	20	AAW50030	Human E27 anti-IgE
39	1008	81.2	218	20	AAW95660	Mus musculus anti-
40	1008	81.2	218	20	AAW95662	Mus musculus anti-
41	1008	81.2	218	21	AAW97472	Amino acid sequenc
42	1008	81.2	218	22	AAW74211	E27 anti-IgE antib
43	1006	81.0	240	20	AAW73875	Human anticirc epsi
44	1005	80.9	218	20	AAW95669	Mus musculus anti-
45	1005	80.9	218	20	AAW95664	Mus musculus anti-

ALIGNMENTS

RESULT 1	
AAW83031	
-ID AAW83031 standard; Protein; 238 AA.	
XX	
AC AAW83031;	
XX	
DT 15-MAR-1999 (first entry)	
XX	
DE Anti-Fas humanised antibody HFE7A light chain HH type.	
XX	
KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;	
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;	
KW systemic lupus erythematosus; graft versus host disease;	
KW Sjogren syndrome; pernicious anaemia; Addison's disease;	
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;	
KW rheumatoid arthritis; autoimmune haemolytic anaemia;	
KW myasthenia gravis; multiple sclerosis; Basedow's disease;	
KW thrombopenia purpura; insulin-dependent diabetes; allergy;	
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy; AIDS;	
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;	
KW transplant rejection; therapy.	
XX	
OS Homo sapiens.	
OS Synthetic.	
XX	
Key Location/Qualifiers	
FT Peptide 1..20	
FT Protein /label= sig_peptide	
FT Protein 21..238	
FT Region /label= Mat_protein	
FT Region 21..131	
FT Region /label= Variable	
FT Region 132..238	
FT Region /label= Constant	

FT Region 44...58
 FT /label= CDR_L1
 FT /note="claim 9"
 FT Region 74...80
 FT /label= CDR_L2
 FT /note="claim 9"
 FT 113...121
 FT /label= CDR_L3
 FT /note="claim 9"
 XX AU9859701-A.
 XX 08-OCT-1998.
 XX 30-MAR-1998; 98AU-0059701.
 XX 08-OCT-1997; 97JP-0276064.
 PR 01-APR-1997; 97JP-0082953.
 PR 25-JUN-1997; 97JP-0169088.
 XX (SANY) SANKYO CO LTD.
 XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX WPI; 1998-543440/47.
 DR N-PSDB; RAV70074.
 XX New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX Claim 21; Page 199-199; 292pp; English.
 XX This is the amino acid sequence of the HH type humanised light
 CC chain of murine anti-human Fas monoclonal antibody HFE7A.
 CC Humanisation of the murine sequence (see AAW83042) entailed making
 CC P47A, K49R, H80S, P81R, V82L, E84P, E85A, A87F and P89V amino acid
 CC substitutions; these residues are conserved in the human light
 CC chain (kappa chain). Host cell Escherichia coli PHSGHH7 SANK 73497
 CC harbors plasmid PHSGHH7 carrying a fusion fragment of the humanised
 CC HH type HFE7A light chain and DNA encoding the region of human
 CC immunoglobulin kappa chain, and is deposited as FERM BP-6073
 CC (claimed). The invention provides methods for producing humanised
 CC antibodies by culturing host cells. Humanised versions of HFE7A
 CC (see AAW83031-37), like native HFE7A, are capable of inducing
 CC apoptosis in abnormal cells expressing Fas, and of inhibiting
 CC Fas-induced apoptosis in normal cells. The humanised antibodies
 CC are used to evaluate, in animal models, treatments of diseases that
 CC involve Fas/Fas ligand interactions, and also to treat such
 CC diseases, including autoimmune disease (e.g. systemic lupus
 CC erythematosus, Hashimoto's disease, graft versus host disease,
 CC Sjogren syndrome, pernicious anaemia, Addison's disease,
 CC scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid
 CC arthritis, autoimmune haemolytic anaemia, sterility, myasthenia
 CC gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura
 CC and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
 XX Sequence 238 AA;
 SQ
 Query Match 100.0%; Score 1242; DB 19; Length 238;
 Best Local Similarity 100.0%; Pred. No. 3.3e-69;
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 METDTILLWLLVWPSTGDIVLTQSPGTLSPGERATLSCRSQSYVDYDGSYMNWY 60
 Db 1 metdtillwllwppstgdivltqspgtlspgeratlsckasqsydydgdsymnw 60
 QY 61 QQKPGQAPRLIIYAASNLESIPDRFSGSGGTDTLTISRLEPADFAVYYCQSNEDPR 120

Db 61 qqkpgqaprlIIyaasnlesgIpdrfsgsgsgtdftltISRLEPADFAVYYCQSNEDPR 120
 QY 121 TFGQGTREIKRTVAAPSVFFPPSPDEQLKSGTASVCLLNFFYREAKVQHKVDNALQS 180
 Db 121 tfgggtreIeIkrtaapsvffppspdeqlksgtasvcllnffypreakvqkvdnalqs 180
 QY 181 GNSQESVTEQDSKDSYSLSTLTLSKADYEKKHYVACEVTHOGLSSPVTKSFNRGEC 238
 Db 181 gnsqesvteqdsksdystlsLTLSKADYEKKHYVACEVTHOGLSSPVTksfnrgec 238
 RESULT 2
 AAB14772
 ID AAB14772 standard; Protein: 238 AA.
 XX AC AAB14772;
 XX DT 24-NOV-2000 (first entry)
 XX DE Humanised anti-Fas antibody light chain, SEQ ID NO:50.
 XX KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; humanised antibody; complementarity determining region; CDR;
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
 KW hepatitis; AIDS; graft rejection; light chain.
 XX Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 OS JP2000169393-A.
 XX 20-JUN-2000.
 XX 30-SEP-1999; 99JP-0278301.
 PR 30-SEP-1998; 98JP-0276883.
 PA (SANY) SANKYO CO LTD.
 DR WPI; 2000-485645/43.
 DR N-PSDB; AAA72124.
 XX Preventive or treating agent for the diseases caused by an abnormality
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody -
 XX Claim 20; Page 78-79; 139pp; Japanese.
 CC The invention relates to compositions for the prevention or treatment
 CC of diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The compositions of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
 CC represent the light chains of several humanised HFE7A-derived anti-Fas
 CC antibodies.
 XX Sequence 238 AA;
 SQ
 Query Match 100.0%; Score 1242; DB 21; Length 238;
 Best Local Similarity 100.0%; Pred. No. 3.3e-69;
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METDTILLVLLWVPGSTGDIIVLTQSPGTLISLSPGERATLSCKASQSDYDGDSDYNNVY 60
 Db 1 metdtillvllwvpgstgdiivltqspgtlslspgeratlsckasqsdvdygdsymvny 60
 QY 61 QOKPGQAPRLIIYAASNLSEGIPIRFGSGSGTDFTLTISRLEPADFAVYQCQSNEDPR 120
 Db 61 qkpgqaprllyaaanlesgipdrfsgsgsgtdftltisrlepafavvyccqsnedpr 120
 QY 121 TFGQGTRLIKRTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQS 180
 Db 121 tfgqgtrleikrtvaapsvfippdeqlksgtasvvcllnnfypreakvqkvdnalqs 180
 QY 181 GNSQSVTEQDSDSTYSLSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 238
 Db 181 gnsqsvteqdsdstyslsstltlskadyekhyacevthqglsspytksfnrgec 238

RESULT 3
 AAW90922 standard; Protein: 238 AA.
 XX
 AC AAW90922;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Humanised anti-Fas antibody HFE7A light chain HH type protein.
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antifertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX
 OS Synthetic.
 XX
 PN EP990663-A2.
 XX
 PD 05-APR-2000.
 XX
 PF 29-SEP-1999; 99EP-0307711.
 XX
 PR 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX
 DR WPI: 2000-258930/23.
 DR N-PSDB; AAA11562.
 XX
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems
 XX
 PS Example reference 14; Page 114-115; 263pp; English.
 XX
 CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antifertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatotropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive

CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A light chain HH type which is used in
 CC the method described in the invention.

XX Sequence 238 AA;

Query Match 100.0%; Score 1242; DB 21; Length 238;
 Best Local Similarity 100.0%; Pred. No. 3.3e-69;
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METDTILLVLLWVPGSTGDIIVLTQSPGTLISLSPGERATLSCKASQSDYDGDSDYNNVY 60
 Db 1 metdtillvllwvpgstgdiivltqspgtlslspgeratlsckasqsdvdygdsymvny 60
 QY 61 QOKPGQAPRLIIYAASNLSEGIPIRFGSGSGTDFTLTISRLEPADFAVYQCQSNEDPR 120
 Db 61 qkpgqaprllyaaanlesgipdrfsgsgsgtdftltisrlepafavvyccqsnedpr 120
 QY 121 TFGQGTRLIKRTVAAPSVFIPPPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQS 180
 Db 121 tfgqgtrleikrtvaapsvfippdeqlksgtasvvcllnnfypreakvqkvdnalqs 180
 QY 181 GNSQSVTEQDSDSTYSLSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 238
 Db 181 gnsqsvteqdsdstyslsstltlskadyekhyacevthqglsspytksfnrgec 238

RESULT 4
 AAW83034 standard; Protein: 238 AA.

XX AC AAW83034;
 XX DT 15-MAR-1999 (first entry)
 XX DE Anti-Fas humanised antibody HFE7A light chain PDHH type.
 XX KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjorgen syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy.

XX OS Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT Peptide 1..20
 FT Protein /label= Sg peptide
 FT Region /label= Mat.protein
 FT 21..238
 FT 21..131

FT Region /label= Variable
 FT 132..238
 FT /label= Constant
 FT Region 44..58
 FT /label= CDR_L1
 FT /note= "claim 9"
 FT 74..80
 FT /label= CDR_L2
 FT /note= "claim 9"
 FT 113..121
 FT /label= CDR_L3
 FT /note= "claim 9"
 FT AU9859701-A.
 PN 08-OCT-1998.
 PD 30-MAR-1998; 98AU-0059701.
 PF 08-OCT-1997; 97JP-0276064.
 PR 01-APR-1997; 97JP-0082953.
 PR 25-JUN-1997; 97JP-0169088.
 XX (SANY) SANKYO CO LTD.
 PA Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX WPI: 1998-543440/47.
 DR N-PSDB; AAV70077.
 PT New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 PS Claim 21; Page 218; 292pp; English.
 XX This is the amino acid sequence of the PDHH type humanised light
 CC chain of murine anti-human Fas monoclonal antibody HFE7A.
 CC Humanisation of the murine sequence (see AAW83042) entailed making
 CC D1E, F47A, K49R, H80S, P81R, V82L, E84P, A87F, T89V and R107K
 CC amino acid substitutions; these residues are conserved in the
 CC human light chain (kappa chain). Host cell Escherichia coli
 CC PHSH5 SANK 70398 harbors plasmid PHSH5 carrying a fusion
 CC fragment of the humanised PDHH type HFE7A light chain and DNA
 CC encoding the region of human immunoglobulin kappa chain, and is
 CC deposited as FERM BP-6274 (claimed). The invention provides
 CC methods for producing humanised antibodies by culturing host
 CC cells. Humanised versions of HFE7A (see AAW83031-37), like native
 CC HFE7A, are capable of inducing apoptosis in abnormal cells
 CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal
 CC cells. The humanised antibodies are used to evaluate, in animal
 CC models, treatments of diseases that involve Fas/Fas ligand
 CC interactions, and also to treat such diseases, including autoimmune
 CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
 CC graft versus host disease, Sjogren syndrome, pernicious anaemia,
 CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
 CC sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
 CC thrombopenia purpura and insulin-dependent diabetes), allergies,
 CC atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
 CC nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
 CC rejection (all claimed).
 XX Sequence 238 AA;
 SQ

Query Match 99.0%; Score 1230; DB 19; Length 238;
 Best Local Similarity 98.7%; Pred. No. 1.8e-68;
 Matches 235; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 METDTILLVLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCSKASQSVVDYDGSYMNWY 60

Db 1 metdtillvllwvpgstgdivltqspgtlslspgeratlsckasqsdydgymnw 60
 Qy 61 QOKPGQAPRLIYAASNLESGTPDRFSGSGCTFTLTISRLEPADFAVYVYCOQSNEDPR 120
 Db 61 qkpgqaprllyaaasnlesgtpdrfsgsgsgtftltisrlepadfavyyccqgsneopr 120
 Qy 121 TFGQGTREIKRTVAAPSVFIFPPSDEQLKSGTASVWCILNNFYPREAKVQWKVDNALQ 180
 Db 121 tfgqgtkiekrtvaapsvfifppsedelksgtasvcllnnfypreakvqwkvdnalq 180
 Qy 181 GNSQSVTEQDQSKDSTYSLSLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238
 Db 181 gnsqsvteqgskdstyslsstltlskadyekhkyvacevthqglsspvtksfnrgec 238

RESULT 5
 AAB14777
 ID AAB14777 standard; Protein: 238 AA.
 AC AAB14777;
 XX 24-NOV-2000 (first entry)
 DT Humanised anti-Fas antibody light chain, SEQ ID NO:107.
 DE Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; humanised antibody; complementarity determining region; CDR;
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
 KW hepatitis; AIDS; graft rejection; light chain.
 XX Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 PN JP2000169393-A.
 XX 20-JUN-2000.
 PD 30-SEP-1999; 99JP-0278301.
 XX 30-SEP-1998; 98JP-0276883.
 PR (SANY) SANKYO CO LTD.
 PA WPI: 2000-485645/43.
 XX N-PSDB; AAA72176.
 DR Preventive or treating agent for the diseases caused by an abnormality
 DR in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody
 PS Claim 20; Page 101; 139pp; Japanese.
 XX The invention relates to compositions for the prevention or treatment
 CC or diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The compositions of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
 CC represent the light chains of several humanised HFE7A-derived anti-Fas
 CC antibodies.
 XX Sequence 238 AA;
 SQ

Query Match 99.0%; Score 1230; DB 21; Length 238;
 Best Local Similarity 98.7%; Pred. No. 1.8e-68;
 Matches 235; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 METDTILLWLLVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSDVDYDGSYNNWY 60
 DQ 1 metdtillwllwpgstgdivltqspgtlsispggeratlsckasqsdvdydgsymnw 60

QY 61 QOKPGQAPRLIYAASNLGSIPIRFGSGSGTDTLTISRLEPADFAVYCCQSNEDPR 120
 DQ 61 qqkpgqaprllyaaanlesgipdrfsgsgsgtdftltisrlepadfavycqsnedpr 120

QY 121 TFGOGTLEIKRTVAAPSVFIPIPPSDQLKSGTASVYVCLLNFFPREAKVQWKVDNALQS 180
 DQ 121 tfgggtkleikrtvaapsvfippsdqlksgtasvycllnffpreakvqwkvdnalqs 180

QY 181 GNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 DQ 181 gnsqesvteqdsksdystlslstltlskadyekhkvacevthqglsspvtksfnrgec 238

RESULT 6
 AAW90927
 ID AAW90927 standard; Protein; 238 AA.
 AC AAW90927;
 DT 08-AUG-2000 (first entry)
 DE Humanised HFE7A designed light chain protein.

KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatologic; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 OS Synthetic.
 XX EP990663-A2.
 PN 05-APR-2000.
 PD 29-SEP-1999; 99EP-0307711.
 XX 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX (SANY) SANKYO CO LTD.
 PA Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX WPI: 2000-258930/23.
 DR N-PSDB; AAA11614.
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems
 PT Claim 3; Page 141-142; 263pp; English.
 PS This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, anti-inflammatory,

CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic); and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A designed light chain which is used in
 CC the method described in the invention.
 XX
 SQ Sequence 238 AA;

Query Match 99.0%; Score 1230; DB 21; Length 238;
 Best Local Similarity 98.7%; Pred. No. 1.8e-68;
 Matches 235; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 METDTILLWLLVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSDVDYDGSYNNWY 60
 DQ 1 metdtillwllwpgstgdivltqspgtlsispggeratlsckasqsdvdydgsymnw 60

QY 61 QOKPGQAPRLIYAASNLGSIPIRFGSGSGTDTLTISRLEPADFAVYCCQSNEDPR 120
 DQ 61 qqkpgqaprllyaaanlesgipdrfsgsgsgtdftltisrlepadfavycqsnedpr 120

QY 121 TFGOGTLEIKRTVAAPSVFIPIPPSDQLKSGTASVYVCLLNFFPREAKVQWKVDNALQS 180
 DQ 121 tfgggtkleikrtvaapsvfippsdqlksgtasvycllnffpreakvqwkvdnalqs 180

QY 181 GNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 DQ 181 gnsqesvteqdsksdystlslstltlskadyekhkvacevthqglsspvtksfnrgec 238

RESULT 7
 AAW83032
 ID AAW83032 standard; Protein; 238 AA.
 XX
 AC AAW83032;
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE Anti-Fas humanised antibody HFE7A light chain HM type.

DE HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy.

XX Homo sapiens.
 OS Synthetic.
 XX
 FT Key Location/Qualifiers
 FT Peptide 1..20

FT Protein /label= Sig_peptide
FT 21..238 /label= Mat_protein
FT 21..131 /label= Variable
FT 132..238 /label= Constant
FT 44..58 /label= CDR_L1
FT /note= "Claim 9"
FT 74..80 /label= CDR_L2
FT /note= "Claim 9"
FT 113..121 /label= CDR_L3
FT /note= "Claim 9"
FN AU9859701-A.
XX 08-OCT-1998.
XX 30-MAR-1998; 98AU-0059701.
XX 08-OCT-1997; 97JP-0276064.
PR 01-APR-1997; 97JP-0082953.
XX 25-JUN-1997; 97JP-0169088.
PA (SANY) SANKYO CO LTD.
XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
XX WPI: 1998-543440/47.
DR N-PSDB; AAV70075.
XX New antibodies and proteins bind conserved epitope of Fas antigen -
PT used to evaluate drugs in animal models and to treat Fas-associated
PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
PT myocarditis, hepatitis and AIDS
XX Claim 21; Page 200; 292pp; English.
XX This is the amino acid sequence of the HM type humanised light
CC chain of murine anti-human Fas monoclonal antibody HFE7A.
CC Humanisation of the murine sequence (see AAW83042) entailed making
CC p47A and K49R amino acid substitutions; these residues are
CC conserved in the human light (kappa) chain. Host cell E. coli
CC PHSGHM17 SANK 73597 harbors plasmid PHSGHM17 carrying a fusion
CC fragment of the humanised HM type HFE7A light chain and DNA
CC encoding the region of human immunoglobulin kappa chain, and is
CC deposited as FERM BP-6072 (claimed). The invention provides
CC methods for producing humanised antibodies by culturing host
CC cells. Humanised versions of HFE7A (see AAW83031-37), like native
CC HFE7A, are capable of inducing apoptosis in abnormal cells
CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal
CC cells. The humanised antibodies are used to evaluate, in animal
CC models, treatments of diseases that involve Fas/Fas ligand
CC interactions, and also to treat such diseases, including autoimmune
CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
CC graft versus host disease, Sjogren syndrome, pernicious anaemia,
CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
CC sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
CC thrombopenia purpura and insulin-dependent diabetes), allergies,
CC atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
CC nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
CC rejection (all claimed).
XX Sequence 238 AA;

Query Match 96.8%; Score 1202; DB 19; Length 238;
Best Local Similarity 97.1%; Pred. No. 9.4e-67;

Matches 231; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy 1 METDTILLWLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCAKASQSVVDVGDSDYMMWY 60
Db 1 metdctillwllwvpgstgdivltqspgtlsispggeratlsckasqsvdvgdsymnw 60
Qy 61 QOKPGQAPRLIYAASNLSEGPDRFSGSGSGTDFTLTISRLEPADFAFYTCQSQSNEPR 120
Db 61 qkpgqaprllyaaanlesgipdrfsgsgsgtdftltihpveedaatyyccsqsnedpr 120
Qy 121 TFGQGTREIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQ 180
Db 121 tfgggtreikrtvaapsvfifppsdeqlksgtasvcllnnfyreakvqwkvdnalqs 180
Qy 181 GNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 gnsqesvteqdsksdystlsstltlskadyekhkvyacevthqglsspvtksfnrgec 238
RESULT 8
AAB14773
ID AAB14773 standard; Protein: 238 AA.
XX AAB14773;
XX AC
XX XX
DT 24-NOV-2000 (first entry)
XX Humanised anti-Fas antibody light chain, SEQ ID NO:52.
XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
KW murine; humanised antibody; complementarity determining region; CDR;
KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
KW hepatitis; AIDS; graft rejection; light chain.
XX Chimeric - Mus musculus.
OS Chimeric - Homo sapiens.
XX JP2000169393-A.
XX 20-JUN-2000.
XX 30-SEP-1999; 99JP-0278301.
XX 30-SEP-1998; 98JP-0276883.
XX (SANY) SANKYO CO LTD.
XX WPI: 2000-485645/43.
DR N-PSDB; AAA72125.
XX Preventive or treating agent for the diseases caused by an abnormality
PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
PT anti-Fas antibody -
XX Claim 20; Page 80-81; 139pp; Japanese.
XX The invention relates to compositions for the prevention or treatment
CC or diseases caused by an abnormality in the Fas/Fas ligand system
CC containing an anti-Fas antibody as the active component. The anti-Fas
CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
CC or a humanised version of HFE7A containing identical CDRs
CC (complementarity determining regions) to antibody HFE7A. Via its
CC interaction with Fas, the antibody of the invention acts as a modulator
CC of apoptosis. The compositions of the invention may therefore be used in
CC the treatment or prevention of conditions such as autoimmune diseases,
CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
CC represent the light chains of several humanised HFE7A-derived anti-Fas
CC antibodies.

SQ Sequence 238 AA;
 Query Match 96.88; Score 1202; DB 21; Length 238;
 Best Local Similarity 97.18; Pred. No. 9.4e-67;
 Matches 231; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 QY 1 METDTLLWLLVPGSTGDIVLTQSPGTLSLSPGERATLSCRKASQSDVDYDGSYMNWY 60
 Db 1 metdtllwllwvpgstgdivltqspgtlspsgeratlsckasqsdvdydgsymnw 60
 QY 61 QOKFGQAPRLIYAASNLSEIPDRFSGSGGTFTLTISRLEPADFAVYYCQSQNEDPR 120
 Db 61 qkqpgqaprllyaaasnlseipdrfsgsggtftltihpveeadaatyycqsqnedpr 120
 QY 121 TFGGTRLEIKRTVAAPSVFPPSDEQLKSGTASVVCLLNNEFPRKAKVQKVDNALQS 180
 Db 121 tfggtrleikrtvaapsvfpppsdeqlksgtasvvcvllnnfpreakvqkvdnalqs 180
 QY 181 GNSQESVTEQDSKDYSLSTLTSLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 Db 181 gnsqesvteqdsksdystltsltlskadyekhkvyacevthqglsspvtksfnrgec 238
 RESULT 9
 AAW90923 ID AAW90923 standard; Protein; 238 AA.
 AC AAW90923;
 DT 08-AUG-2000 (first entry)
 XX Humanised anti-Fas antibody HFE7A light chain HM type protein.
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiartherosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 OS Synthetic.
 XX EP990663-A2.
 XX 05-APR-2000.
 XX 29-SEP-1999; 99EP-0307711.
 XX 30-SEP-1998; 98JP-0276881.
 XX 30-SEP-1998; 98JP-0276882.
 XX (SANY) SANKYO CO LTD.
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX WPI; 2000-258930/23.
 DR N-PSDB; AAA11563.
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems -
 XX Example reference 14; Page 117-118; 263pp; English.
 CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents

CC apoptosis in cells with abnormal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiartherosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A light chain HM type which is used in
 CC the method described in the invention.
 XX
 SQ Sequence 238 AA;

Query Match 96.88; Score 1202; DB 21; Length 238;
 Best Local Similarity 97.18; Pred. No. 9.4e-67;
 Matches 231; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 QY 1 METDTLLWLLVPGSTGDIVLTQSPGTLSLSPGERATLSCRKASQSDVDYDGSYMNWY 60
 Db 1 metdtllwllwvpgstgdivltqspgtlspsgeratlsckasqsdvdydgsymnw 60
 QY 61 QOKFGQAPRLIYAASNLSEIPDRFSGSGGTFTLTISRLEPADFAVYYCQSQNEDPR 120
 Db 61 qkqpgqaprllyaaasnlseipdrfsgsggtftltihpveeadaatyycqsqnedpr 120
 QY 121 TFGGTRLEIKRTVAAPSVFPPSDEQLKSGTASVVCLLNNEFPRKAKVQKVDNALQS 180
 Db 121 tfggtrleikrtvaapsvfpppsdeqlksgtasvvcvllnnfpreakvqkvdnalqs 180
 QY 181 GNSQESVTEQDSKDYSLSTLTSLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 Db 181 gnsqesvteqdsksdystltsltlskadyekhkvyacevthqglsspvtksfnrgec 238
 RESULT 10
 AAW83035 ID AAW83035 standard; Protein; 238 AA.
 XX AAW83035;
 XX 15-MAR-1999 (first entry)
 XX Anti-Fas humanised antibody HFE7A light chain PDHM type.
 XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjorgen syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW glomerular nephritis; myocarditis; cardiomyopathy;
 KW transplant rejection; hepatitis; AIDS;
 XX Homo sapiens.
 OS Synthetic.

XX FH Key Location/Qualifiers
 FT Peptide 1..20
 FT Protein /label= Sig_peptide
 FT Region 21..238
 FT Region /label= Mat_protein
 FT Region 21..131
 FT Region /label= Variable
 FT Region 132..238
 FT Region /label= Constant
 FT Region 44..58
 FT Region /label= CDR_L1
 FT Region /note= "claim 9"
 FT Region 74..80
 FT Region /label= CDR_L2
 FT Region /note= "claim 9"
 FT Region 113..121
 FT Region /label= CDR_L3
 FT Region /note= "claim 9"
 PN AU9859701-A.
 PD 08-OCT-1998.
 XX 30-MAR-1998; 98AU-0059701.
 XX 08-OCT-1997; 97JP-0276064.
 PR 01-APR-1997; 97JP-0082953.
 PR 25-JUN-1997; 97JP-0169088.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 PI Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX
 DR WPI; 1998-543440/47.
 DR N-PSDB; RAV70078.
 XX
 PT New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX
 PS Claim 21; Page 220-221; 292pp; English.
 XX
 CC This is the amino acid sequence of the PDHM type humanised light
 CC chain of murine anti-human Fas monoclonal antibody HFE7A.
 CC Humanisation of the murine sequence (see AAW83042) entailed making
 CC D1E, P47A, K49R and R107K amino acid substitutions; these
 CC residues are conserved in the human light (kappa) chain. Host
 CC cell Escherichia coli pSHM2 SANK 70198 harbors plasmid pSHM2
 CC carrying a fusion of the humanised PDHM type HFE7A light chain and
 CC DNA encoding the region of human immunoglobulin kappa chain, and is
 CC deposited as FERM BP-6272 (claimed). The invention provides
 CC methods for producing humanised antibodies by culturing host
 CC cells. Humanised versions of HFE7A (see AAW83031-37), like native
 CC HFE7A, are capable of inducing apoptosis in abnormal cells
 CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal
 CC cells. The humanised antibodies are used to evaluate, in animal
 CC models, treatments of diseases that involve Fas/Fas ligand
 CC interactions, and also to treat such diseases, including autoimmune
 CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
 CC graft versus host disease, Sjogren syndrome, pernicious anaemia,
 CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
 CC sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
 CC thrombopenia purpura and insulin-dependent diabetes), allergies,
 CC atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
 CC nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
 CC rejection (all claimed).
 XX
 SQ Sequence 238 AA;

Query Match 96.2%; Score 1195; DB 19; Length 238;
 Best Local Similarity 96.2%; Pred. No. 2.5e-66;
 Matches 229; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 METDTILLWLLVWPGSTGDIVLTQSPGTLSLSPGERATLSCAKASQSYVDYDGSYMMWY 60
 Db 1 metdtillwllwvpgstgdivltqspgtlspsgeratlsckasqsdydgdsgymwy 60
 Qy 61 QOKPQAPRLIIYAASNLSEGIPTDFRFGSGSGCTDFTLIRLEPADFAVYICQNSNEDPR 120
 Db 61 qgkpgqaprlIIyaasnlesgipdrfsgsgsgtdftlirhpveeedaatyyccgsgnedpr 120
 Qy 121 TFGGTRLEIKRTVAAPSVFFIPPPDEOLKSGTASVWCLLNFFYPREAKVQKVDNALQS 180
 Db 121 tfggtrleikrtvaapsvffippsdeqlksgtasvcllnmfypreakvqkvdnalqs 180
 Qy 181 GNSQSVTEQDSKDYSLSTLTLSKADYEKHKYVACEVTHQGLSSPVTKSFNRGEC 238
 Db 181 gnsqsvteqgskdstyslsstltlskadyekhkvyacevthqglsspvtksfnrgec 238
 RESULT 11
 AAB14778
 ID AAB14778 standard; Protein: 238 AA.
 XX
 AC AAB14778;
 XX
 DT 24-NOV-2000 (first entry)
 XX
 DE Humanised anti-Fas antibody light chain, SEQ ID NO:109.
 XX
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; humanised antibody; complementarity determining region; CDR;
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
 KW hepatitis; AIDS; graft rejection; light chain.
 XX
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX
 PN JP2000169393-A.
 XX
 PD 20-JUN-2000.
 XX
 PF 30-SEP-1999; 99JP-0278301.
 XX
 PR 30-SEP-1998; 98JP-0276883.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 DR WPI; 2000-485645/43.
 DR N-PSDB; AAA72177.
 XX
 PT Preventive or treating agent for the diseases caused by an abnormality
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody -
 XX
 PS Claim 20; Page 103; 139pp; Japanese.
 XX
 CC The invention relates to compositions for the prevention or treatment
 CC of diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The compositions of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778

CC represent the light chains of several humanised HFE7A-derived anti-Fas
 CC antibodies.
 XX

SQ Sequence 238 AA;

Query Match 96.2%; Score 1195; DB 21; Length 238;

Best Local Similarity 96.2%; Pred. No. 2.5e-66;

Matches 229; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 METDTILLWLLWVPGSGDIVLTQSPGTLSPGERTATLSCKASQSDVDYDGDSYNNWY 60

DB 1 MECTDTILLWLLWVPGSGDIVLTQSPGTLSPGERTATLSCKASQSDVDYDGDSYNNWY 60

QY 61 QORPGAPRLIIYAANLSEGIPIPRFSGSGGTDFTLTISRLEPADFAVYVYCOQSNEDPR 120

DB 61 QKPGGAPRLIIYAANLSEGIPIPRFSGSGGTDFTLTISRLEPADFAVYVYCOQSNEDPR 120

QY 121 TFGQGRLEIKRTVAAPSVFIIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180

DB 121 TFGQGRLEIKRTVAAPSVFIIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180

QY 181 GNSQESVTEODSKDYSISSTLTLSKADYKHKVYACEVTHOGLSPVTKSFNRGEC 238

DB 181 GNSQESVTEODSKDYSISSTLTLSKADYKHKVYACEVTHOGLSPVTKSFNRGEC 238

RESULT 12

AAW90928

ID AAW90928 standard; Protein; 238 AA.

AC AAW90928;

XX

DT 08-AUG-2000 (first entry)

XX

DE Humanised HFE7A designed light chain protein #2.

XX

KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

OS Synthetic.

XX

XX EP990663-A2.

XX

PN 05-APR-2000.

XX

PF 29-SEP-1999; 99PP-0307711.

XX

PR 30-SEP-1998; 98JP-0276881.

XX

PR 30-SEP-1998; 98JP-0276882.

XX

PA (SANY) SANKYO CO LTD.

XX

PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

XX

DR WPI: 2000-258930/23.

DR N-PSDB; AAL1615.

XX

PT New humanized anti-Fas antibody, useful for treating or preventing e.g.

PT inflammatory or autoimmune disease, induces apoptosis selectively in

PT cells with abnormal Fas-Fas ligand systems

XX

PS Example reference 21; Page 144-145; 263pp; English.

XX

CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with abnormal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A designed light chain which is used in
 CC the method described in the invention.

XX Sequence 238 AA;

Query Match 96.2%; Score 1195; DB 21; Length 238;

Best Local Similarity 96.2%; Pred. No. 2.5e-66;

Matches 229; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 METDTILLWLLWVPGSGDIVLTQSPGTLSPGERTATLSCKASQSDVDYDGDSYNNWY 60

DB 1 MECTDTILLWLLWVPGSGDIVLTQSPGTLSPGERTATLSCKASQSDVDYDGDSYNNWY 60

QY 61 QORPGAPRLIIYAANLSEGIPIPRFSGSGGTDFTLTISRLEPADFAVYVYCOQSNEDPR 120

DB 61 QKPGGAPRLIIYAANLSEGIPIPRFSGSGGTDFTLTISRLEPADFAVYVYCOQSNEDPR 120

QY 121 TFGQGRLEIKRTVAAPSVFIIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180

DB 121 TFGQGRLEIKRTVAAPSVFIIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180

QY 181 GNSQESVTEODSKDYSISSTLTLSKADYKHKVYACEVTHOGLSPVTKSFNRGEC 238

DB 181 GNSQESVTEODSKDYSISSTLTLSKADYKHKVYACEVTHOGLSPVTKSFNRGEC 238

RESULT 13

AAW83033

ID AAW83033 standard; Protein; 238 AA.

XX

AC AAW83033;

XX

DT 15-MAR-1999 (first entry)

XX

XX

XX Anti-Fas humanised antibody HFE7A light chain MM type.

XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;

KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;

KW systemic lupus erythematosus; graft versus host disease;

KW Sjogren syndrome; pernicious anaemia; Addison's disease;

KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;

KW rheumatoid arthritis; autoimmune hemolytic anaemia;

KW myasthenia gravis; multiple sclerosis; Basedow's disease;

KW thrombopenia purpura; insulin-dependent diabetes; allergy;

KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;

KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;

KW transplant rejection; therapy.

XX OS Homo sapiens.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Peptide 1..20
 FT Protein /label= Sig_peptide
 FT 21..238
 FT Region /label= Mat_protein
 FT 21..131
 FT Region /label= Variable
 FT 132..238
 FT Region /label= Constant
 FT 44..58
 FT Region /label= CDR_L1
 FT /note= "claim 9"
 FT Region 74..80
 FT /label= CDR_L2
 FT /note= "claim 9"
 FT Region 113..121
 FT /label= CDR_L3
 FT /note= "claim 9"
 XX
 PN AU9859701-A.
 XX
 XX 08-OCT-1998.
 XX
 XX 30-MAR-1998; 98AU-0059701.
 XX
 PR 08-OCT-1997; 97JP-0276064.
 PR 01-APR-1997; 97JP-0082953.
 PR 25-JUN-1997; 97JP-0169088.
 XX
 XX (SANY) SANKYO CO LTD.
 XX
 PI Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX
 DR WPI: 1998-543440/47.
 DR N-PSDB; AAV70076.
 XX
 PT New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX
 PS Claim 21; Page 202; 292pp; English.
 XX
 CC This is the amino acid sequence of the MM type humanised light
 CC chain of murine anti-human Fas monoclonal antibody HFE7A. E. coli
 CC SANK 73697 harbors plasmid pHS6M6 carrying a fusion fragment of the
 CC humanised MM type HFE7A light chain and DNA encoding the region of
 CC human kappa chain, and is deposited as FERM BP-6071 (claimed). The
 CC invention provides methods for producing humanised antibodies by
 CC culturing host cells. Humanised versions of HFE7A (see AAW83031-37),
 CC like native HFE7A, are capable of inducing apoptosis in abnormal
 CC cells expressing Fas, and of inhibiting Fas-induced apoptosis in
 CC normal cells. The humanised antibodies are used to evaluate, in
 CC animal models, treatments of diseases that involve Fas/Fas ligand
 CC interactions, and also to treat such diseases, including autoimmune
 CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
 CC graft versus host disease, Sjogren syndrome, pernicious anaemia,
 CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
 CC sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
 CC thrombopenia purpura and insulin-dependent diabetes), allergies,
 CC atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
 CC nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
 CC rejection (all claimed).
 XX
 SQ Sequence 238 AA;

Query Match 96.1%; Score 1194; DB 19; Length 238;
 Best Local Similarity 96.2%; Pred. No. 2.9e-66;
 Matches 229; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 Qy 1 METDTILLWVLLWVPGSTGDIVLTQSPGTLISLSPGERATLSCAKASQSVVDGDSYMMWY 60
 Db 1 metdtillwvllwvpgstgdivltqspgtlislspgeratlsckasqsvdydgdsmwmy 60
 Qy 61 QOKPGQAPRLIIYAASNLGCIPIRFSGSGSGTDTLTISRLPADFAVYYCQSQSNEDPR 120
 Db 61 qkpgqpkliliyaasnlesgipdrfsgsgsgtdftltihpveedaatyycqgsnedpr 120
 Qy 121 TFGGTRLEIKRTVAAPSVFPPSPDEOLKSGTASVVCLLNNFYPRKAKVQKVDNALQS 180
 Db 121 tfggtrleikrtvaapsvfppspdeqlksgtasvvcllnnfypreakvqkvdnalqs 180
 Qy 181 GNSQESVTEQDSKDYSLSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNKGEC 238
 Db 181 gnsqesvteqdsksdystlsstltlskadyekhkvyacevthqglsspvtksfnrgec 238
 RESULT 14
 AAB14774
 ID AAB14774 standard; Protein: 238 AA.
 XX
 AC AAB14774;
 XX
 DT 24-NOV-2000 (first entry)
 XX
 DE Humanised anti-Fas antibody light chain, SEQ ID NO:54.
 DE
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; humanised antibody; complementarity determining region; CDR;
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
 KW hepatitis; AIDS; graft rejection; light chain.
 XX
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX
 PN JP2000169393-A.
 XX
 XX 20-JUN-2000.
 XX
 XX 30-SEP-1999; 99JP-0278301.
 XX
 XX 30-SEP-1998; 98JP-0276883.
 XX
 XX (SANY) SANKYO CO LTD.
 XX
 DR WPI: 2000-485645/43.
 DR N-PSDB; AAA72126.
 XX
 PT Preventive or treating agent for the diseases caused by an abnormality
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody
 XX
 PS Claim 20; Page 83; 139pp; Japanese.
 XX
 CC The invention relates to compositions for the prevention or treatment
 CC of diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementary determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The compositions of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
 CC represent the light chains of several humanised HFE7A-derived anti-Fas

```

CC antibodies.
XX Sequence 238 AA;
SQ

Query Match 96.1%; Score 1194; DB 21; Length 238;
Best Local Similarity 96.2%; Pred. No. 2.9e-66;
Matches 229; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 METDTILLWVLLWPGSTGDIVLTQSPGTLISLSPGERATLISCKASQSDVDGDSYMNWY 60
Db 1 metdtillwvllwpgstgdivltqspgtlislspgeratlsckasqsdvdygdsymnw 60
Qy 61 OOKPGQAPRLTIYAASNLIESGIPDRFSGSGCTDFTLTISRLEPADFAVYVYQQSNEDPR 120
Db 61 qgkpgqpkllyaaanlesgipdrfsgsgctdftltihpveedaatyycqgsnedpr 120
Qy 121 TFGQGTREIKRTVAAPSVFIFPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQ 180
Db 121 tfgggtrleikrtvaapsvfifppdsedqlksgtasvvcvllnnfypreakvqkvdnalq 180
Qy 181 GNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 gnsqesvteqdsksstyslsstltlskadyekhkvyacevthqglsspvtksfnrgec 238

RESULT 15
AAW90924
ID AAW90924 standard; Protein; 238 AA.
XX
AC AAW90924;
XX
DT 08-AUG-2000 (first entry)
XX
DE Humanised anti-Fas antibody HFE7A light chain MM type protein.
XX
KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
KW dermatologic; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX
OS Synthetic.
XX
EP990663-A2.
XX
05-APR-2000.
XX
29-SEP-1999; 99EP-0307711.
XX
30-SEP-1998; 98JP-0276881.
XX
30-SEP-1998; 98JP-0276882.
XX
(SANY ) SANKYO CO LTD.
XX
Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX
WPI: 2000-258930/23.
XX
N-PSDB; AAA11564.
XX
New humanized anti-Fas antibody, useful for treating or preventing e.g.
XX inflammatory or autoimmune disease, induces apoptosis selectively in
XX cells with abnormal Fas-Fas ligand systems
XX
Example reference 14; Page 119-120; 263pp; English.
XX
This invention describes a novel humanized anti-Fas antibody-like

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CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, immunosuppressive, thyromimetic,
CC immunomodulatory, dermatologic, antiinfertility, neuroprotective,
CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
CC antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Sjorgen's syndrome, rheumatoid arthritis, graft
CC versus host disease, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC anemia, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a humanised anti-Fas antibody HFE7A light chain MM type which is used in
CC the method described in the invention.
XX
SQ Sequence 238 AA;

```

```

Query Match 96.1%; Score 1194; DB 21; Length 238;
Best Local Similarity 96.2%; Pred. No. 2.9e-66;
Matches 229; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 METDTILLWVLLWPGSTGDIVLTQSPGTLISLSPGERATLISCKASQSDVDGDSYMNWY 60
Db 1 metdtillwvllwpgstgdivltqspgtlislspgeratlsckasqsdvdygdsymnw 60
Qy 61 OOKPGQAPRLTIYAASNLIESGIPDRFSGSGCTDFTLTISRLEPADFAVYVYQQSNEDPR 120
Db 61 qgkpgqpkllyaaanlesgipdrfsgsgctdftltihpveedaatyycqgsnedpr 120
Qy 121 TFGQGTREIKRTVAAPSVFIFPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQ 180
Db 121 tfgggtrleikrtvaapsvfifppdsedqlksgtasvvcvllnnfypreakvqkvdnalq 180
Qy 181 GNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 gnsqesvteqdsksstyslsstltlskadyekhkvyacevthqglsspvtksfnrgec 238

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Search completed: April 24, 2002, 15:09:51
Job time: 94 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run On: April 24, 2002, 15:08:17 ; Search time 42.08 seconds
(without alignments)
127.276 Million cell updates/sec

Title: US-09-499-662-50
Perfect score: 1242
Sequence: 1 MEYDTILLWVLLWVPESTG.....EVTHQGLSSPVTKSFNRGEC 238

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
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2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
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4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
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6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1045	84.1	218	5	PCT-US96-13152-2
2	1031	83.0	218	2	US-08-887-352B-13
3	1031	83.0	218	3	US-08-466-151-9
4	1031	83.0	218	4	US-09-109-207C-13
5	1031	83.0	218	4	US-09-296-005-13
6	1008	81.2	218	4	US-09-282-505-1
7	1008	81.2	218	4	US-09-054-235-1
8	1005	80.9	218	2	US-08-887-352B-15
9	1005	80.9	218	2	US-08-887-352B-17
10	1005	80.9	218	2	US-08-887-352B-19
11	1005	80.9	218	2	US-08-887-352B-24
12	1005	80.9	218	4	US-09-109-207C-15
13	1005	80.9	218	4	US-09-109-207C-17
14	1005	80.9	218	4	US-09-109-207C-19
15	1005	80.9	218	4	US-09-109-207C-24
16	1005	80.9	218	4	US-09-296-005-15
17	1005	80.9	218	4	US-09-296-005-17
18	1005	80.9	218	4	US-09-296-005-19
19	1005	80.9	218	4	US-09-296-005-24
20	974.5	78.5	241	2	US-07-916-098A-56
21	970	78.1	234	4	US-09-049-672A-6
22	964.5	77.7	239	3	US-08-487-550-6
23	954.5	76.9	235	1	US-08-276-852-153
24	954.5	76.9	235	1	US-08-899-575-153
25	954.5	76.9	235	1	US-08-899-575-153
26	954.5	76.9	235	5	PCT-US95-08743-153
27	953.5	76.8	233	2	US-07-934-373C-25

28	953.5	76.8	233	3	US-08-437-642B-25	Sequence 25, Appl
29	953.5	76.8	233	5	PCT-US93-07832-25	Sequence 25, Appl
30	950	76.5	214	2	US-07-934-373C-39	Sequence 39, Appl
31	950	76.5	214	3	US-08-437-642B-39	Sequence 39, Appl
32	950	76.5	214	5	PCT-US93-07832-39	Sequence 39, Appl
33	950	76.5	236	1	US-08-157-101A-5	Sequence 5, Appl
34	947.5	76.3	214	2	US-08-480-753-6	Sequence 6, Appl
35	947.5	76.3	214	3	US-09-041-889-11	Sequence 11, Appl
36	947.5	76.3	214	3	US-08-837-058-11	Sequence 11, Appl
37	946.5	76.2	235	4	US-09-171-945-97	Sequence 97, Appl
38	945	76.1	214	2	US-07-934-373C-40	Sequence 40, Appl
39	945	76.1	214	2	US-08-788-800-11	Sequence 11, Appl
40	945	76.1	214	3	US-08-437-642B-40	Sequence 40, Appl
41	945	76.1	214	3	US-09-097-309-2	Sequence 2, Appl
42	945	76.1	214	4	US-09-097-171A-2	Sequence 2, Appl
43	945	76.1	214	5	PCT-US93-07832-40	Sequence 40, Appl
44	945	76.1	237	3	US-09-097-309-6	Sequence 6, Appl
45	945	76.1	237	4	US-09-097-171A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
PCT-US96-13152-2
; Sequence 2, Application PC/TUS9613152
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich, et al.
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; ADDRESSEE: Attn: Norman D. Hanson
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13152
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: 27-Dec-95
; APPLICATION NUMBER: EP 95 112 895.8
; FILING DATE: 17-Aug-95
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 19-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Norman D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-13152-2

Query Match 84.1%; Score 1045; DB 5; Length 218;
Best Local Similarity 90.8%; Pred. No. 3.9e-82;

QY 141 IFPPSDEOLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 200
Db 121 IFPPSDEOLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
QY 201 STLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 4

US-09-109-207C-13
; Sequence 13, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-13

Query Match 83.0%; Score 1031; DB 4; Length 218;
Best Local Similarity 89.4%; Pred. No. 6.1e-81;
Matches 195; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 21 DIVLTQSPGTLISLSPGERATLSCAKASQVDYDGSYMNWYQKPGQAPRLIIYAASNLES 80
Db 1 DIQLTQSPSSLASVGDRTITCRASQSDYDGSYMNWYQKPGKAPKLLIIYAASYLE 60
QY 81 GIPDRFSGSGGTDFLTISRLEPADFAVYYCQSNEDPRTFGQGTREIKRTVAAPSVF 140
Db 61 GVPDRFSGSGGTDFLTISRLEPADFAVYYCQSHEDPRTFGQGTREIKRTVAAPSVF 120
QY 141 IFPPSDEOLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 200
Db 121 IFPPSDEOLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
QY 201 STLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 5

US-09-296-005-13
; Sequence 13, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial

; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-296-005-13

Query Match 83.0%; Score 1031; DB 4; Length 218;
Best Local Similarity 89.4%; Pred. No. 6.1e-81;
Matches 195; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 21 DIVLTQSPGTLISLSPGERATLSCAKASQVDYDGSYMNWYQKPGQAPRLIIYAASNLES 80
Db 1 DIQLTQSPSSLASVGDRTITCRASQSDYDGSYMNWYQKPGKAPKLLIIYAASYLE 60
QY 81 GIPDRFSGSGGTDFLTISRLEPADFAVYYCQSNEDPRTFGQGTREIKRTVAAPSVF 140
Db 61 GVPDRFSGSGGTDFLTISRLEPADFAVYYCQSHEDPRTFGQGTREIKRTVAAPSVF 120
QY 141 IFPPSDEOLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 200
Db 121 IFPPSDEOLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
QY 201 STLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 6

US-09-282-505-1
; Sequence 1, Application US/09282505A
; Patent No. 6194551
; GENERAL INFORMATION:
; APPLICANT: Esho Ekinaduse Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R1
; CURRENT APPLICATION NUMBER: US/09/282,505A
; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-218
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6194551
US-09-282-505-1

Query Match 81.2%; Score 1008; DB 4; Length 218;
Best Local Similarity 87.6%; Pred. No. 5.7e-79;
Matches 191; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 21 DIVLTQSPGTLISLSPGERATLSCAKASQVDYDGSYMNWYQKPGQAPRLIIYAASNLES 80
Db 1 DIQLTQSPSSLASVGDRTITCRASQSDYDGSYMNWYQKPGKAPKLLIIYAASYLE 60
QY 81 GIPDRFSGSGGTDFLTISRLEPADFAVYYCQSNEDPRTFGQGTREIKRTVAAPSVF 140
Db 61 GVPDRFSGSGGTDFLTISRLEPADFAVYYCQSHEDPRTFGQGTREIKRTVAAPSVF 120
QY 141 IFPPSDEOLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 200
Db 121 IFPPSDEOLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
QY 201 STLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 7

US-09-054-255-1
; Sequence 1, Application US/09054255

Patent No. 6242195
; GENERAL INFORMATION:
; APPLICANT: Escho Ekinaduse Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266
; CURRENT APPLICATION NUMBER: US/09/054,255
; CURRENT FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: E27 anti-IgE antibody light chain
US-09-054-255-1

Query Match 81.2%; Score 1008; DB 4; Length 218;
Best Local Similarity 87.6%; Pred. No. 5.7e-79;
Matches 191; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 21 DIVLTQSPGTLSPGERATLSCCKASQSDYDGDSDYNNYQKPGQAPRLIIYAASNLES 80
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGEGDSYNNYQKPGKAPKLLIIYAASYLE 60
QY 81 GIPDRFSGSGGTDFLTISRLEPAFADFAVYCCQSNEDPRTFGQGRLEIKRTVAAPSVF 140
Db 61 GVPFRSGSGGTDFLTISRLEPAFADFAVYCCQSHEDPYTFGQGRLEIKRTVAAPSVF 120
QY 141 IFPPSEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYSLS 200
Db 121 IFPPSEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYSLS 180
QY 201 STLTLSKADYKHKVYACEVTHQGLSSPTKSFNRGEC 238
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPTKSFNRGEC 218

RESULT 8
US-08-887-352B-15
; Sequence 15, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiue, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-17

Query Match 80.9%; Score 1005; DB 2; Length 218;
Best Local Similarity 87.2%; Pred. No. 1e-78;
Matches 190; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

QY 21 DIVLTQSPGTLSPGERATLSCCKASQSDYDGDSDYNNYQKPGQAPRLIIYAASNLES 80
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGEGDSYNNYQKPGKAPKLLIIYAASYLE 60
QY 81 GIPDRFSGSGGTDFLTISRLEPAFADFAVYCCQSNEDPRTFGQGRLEIKRTVAAPSVF 140
Db 61 GVPFRSGSGGTDFLTISRLEPAFADFAVYCCQSHEDPYTFGQGRLEIKRTVAAPSVF 120
QY 141 IFPPSEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYSLS 200
Db 121 IFPPSEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYSLS 180
QY 201 STLTLSKADYKHKVYACEVTHQGLSSPTKSFNRGEC 238
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPTKSFNRGEC 218

RESULT 9
US-08-887-352B-17
; Sequence 17, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiue, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-17

Query Match 80.9%; Score 1005; DB 2; Length 218;
Best Local Similarity 87.2%; Pred. No. 1e-78;
Matches 190; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

QY 21 DIVLTQSPGTLSPGERATLSCCKASQSDYDGDSDYNNYQKPGQAPRLIIYAASNLES 80
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGEGDSYNNYQKPGKAPKLLIIYAASYLE 60
QY 81 GIPDRFSGSGGTDFLTISRLEPAFADFAVYCCQSNEDPRTFGQGRLEIKRTVAAPSVF 140
Db 61 GVPFRSGSGGTDFLTISRLEPAFADFAVYCCQSHEDPYTFGQGRLEIKRTVAAPSVF 120
QY 141 IFPPSEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYSLS 200
Db 121 IFPPSEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYSLS 180
QY 201 STLTLSKADYKHKVYACEVTHQGLSSPTKSFNRGEC 238
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPTKSFNRGEC 218

;; PRIOR APPLICATION NUMBER: US 60/051,554
;; PRIOR FILING DATE: 1997-07-03
;; NUMBER OF SEQ ID NOS: 44
;; SEQ ID NO 15
;; LENGTH: 218
;; TYPE: PRT
;; ORGANISM: Artificial
;; FEATURE:
;; NAME/KEY: Artificial
;; LOCATION: 1-218
;; OTHER INFORMATION: Light chain sequence derived from MAEL1
US-09-109-207C-15

Query Match 80.9%; Score 1005; DB 4; Length 218;
Best Local Similarity 87.2%; Pred. No. 1e-78; Indels 0; Gaps 0;
Matches 190; Conservative 15; Mismatches 13;
Qy 21 DIVLTQSPGCTLSLSPGERATLSCAKSQSYVDYDGDSDYMMWYQKPGQAPRLLIYAASNL 80
Db 1 DIQLTQSPSSLSASVGDRTITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
Qy 81 GIPDRFSGSGGTDTLTISRLEPADFAVYYCQQSNEDPRFTGQGRLEIKRTVAAPSVF 140
Db 61 GVPFRSGSGGTDTLTISRLEPADFAVYYCQQSNEDPRFTGQGRLEIKRTVAAPSVF 120
Qy 141 IFPPSDEQLKSGTASVCLNNFYPRKAVQKVDNALQSGNSQESVTEQDSKDSYSL 200
Db 121 IFPPSDEQLKSGTASVCLNNFYPRKAVQKVDNALQSGNSQESVTEQDSKDSYSL 180
Qy 201 STLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 218

RESULT 13
US-09-109-207C-17
;; Sequence 17, Application US/09109207C
;; Patent No. 6172213
;; GENERAL INFORMATION:
;; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
;; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
;; FILE REFERENCE: P1123R1
;; CURRENT APPLICATION NUMBER: US/09/109,207C
;; CURRENT FILING DATE: 1998-06-30
;; PRIOR APPLICATION NUMBER: US 60/051,554
;; PRIOR FILING DATE: 1997-07-03
;; NUMBER OF SEQ ID NOS: 44
;; SEQ ID NO 17
;; LENGTH: 218
;; TYPE: PRT
;; ORGANISM: Artificial
;; FEATURE:
;; NAME/KEY: Artificial
;; LOCATION: 1-218
;; OTHER INFORMATION: Light chain sequence derived from MAEL1
US-09-109-207C-17

Query Match 80.9%; Score 1005; DB 4; Length 218;
Best Local Similarity 87.2%; Pred. No. 1e-78;
Matches 190; Conservative 15; Mismatches 13; Indels 0; Gaps 0;
Qy 21 DIVLTQSPGCTLSLSPGERATLSCAKSQSYVDYDGDSDYMMWYQKPGQAPRLLIYAASNL 80
Db 1 DIQLTQSPSSLSASVGDRTITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
Qy 81 GIPDRFSGSGGTDTLTISRLEPADFAVYYCQQSNEDPRFTGQGRLEIKRTVAAPSVF 140
Db 61 GVPFRSGSGGTDTLTISRLEPADFAVYYCQQSNEDPRFTGQGRLEIKRTVAAPSVF 120
Qy 141 IFPPSDEQLKSGTASVCLNNFYPRKAVQKVDNALQSGNSQESVTEQDSKDSYSL 200
Db 121 IFPPSDEQLKSGTASVCLNNFYPRKAVQKVDNALQSGNSQESVTEQDSKDSYSL 180

Db 121 IFPPSDEQLKSGTASVCLNNFYPRKAVQKVDNALQSGNSQESVTEQDSKDSYSL 180
Qy 201 STLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 218
RESULT 14
US-09-109-207C-19
;; Sequence 19, Application US/09109207C
;; Patent No. 6172213
;; GENERAL INFORMATION:
;; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
;; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
;; FILE REFERENCE: P1123R1
;; CURRENT APPLICATION NUMBER: US/09/109,207C
;; CURRENT FILING DATE: 1998-06-30
;; PRIOR APPLICATION NUMBER: US 60/051,554
;; PRIOR FILING DATE: 1997-07-03
;; NUMBER OF SEQ ID NOS: 44
;; SEQ ID NO 19
;; LENGTH: 218
;; TYPE: PRT
;; ORGANISM: Artificial
;; FEATURE:
;; NAME/KEY: Artificial
;; LOCATION: 1-218
;; OTHER INFORMATION: Light chain F(ab) sequence derived from MAEL1
US-09-109-207C-19

Query Match 80.9%; Score 1005; DB 4; Length 218;
Best Local Similarity 87.2%; Pred. No. 1e-78; Indels 0; Gaps 0;
Matches 190; Conservative 15; Mismatches 13;
Qy 21 DIVLTQSPGCTLSLSPGERATLSCAKSQSYVDYDGDSDYMMWYQKPGQAPRLLIYAASNL 80
Db 1 DIQLTQSPSSLSASVGDRTITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
Qy 81 GIPDRFSGSGGTDTLTISRLEPADFAVYYCQQSNEDPRFTGQGRLEIKRTVAAPSVF 140
Db 61 GVPFRSGSGGTDTLTISRLEPADFAVYYCQQSNEDPRFTGQGRLEIKRTVAAPSVF 120
Qy 141 IFPPSDEQLKSGTASVCLNNFYPRKAVQKVDNALQSGNSQESVTEQDSKDSYSL 200
Db 121 IFPPSDEQLKSGTASVCLNNFYPRKAVQKVDNALQSGNSQESVTEQDSKDSYSL 180
Qy 201 STLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 218

RESULT 15
US-09-109-207C-24
;; Sequence 24, Application US/09109207C
;; Patent No. 6172213
;; GENERAL INFORMATION:
;; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
;; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
;; FILE REFERENCE: P1123R1
;; CURRENT APPLICATION NUMBER: US/09/109,207C
;; CURRENT FILING DATE: 1998-06-30
;; PRIOR APPLICATION NUMBER: US 60/051,554
;; PRIOR FILING DATE: 1997-07-03
;; NUMBER OF SEQ ID NOS: 44
;; SEQ ID NO 24
;; LENGTH: 218
;; TYPE: PRT
;; ORGANISM: Artificial
;; FEATURE:
;; NAME/KEY: Artificial
;; LOCATION: 1-218
;; OTHER INFORMATION: Light chain F(ab)'2 sequence derived from MAEL1

US-09-109-207C-24

Query Match 80.9%; Score 1005; DB 4; Length 218;
Best Local Similarity 87.2%; Pred. No. 1e-78;
Matches 190; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

QY	21	DIYLTQSPGTLTSLSPGERATLSCAKSQSDYDGDSYMNNYQOKPGQAPRLIIYAASNLES	80
Db	1	DIQLTQSPSLSASVGDRTTTCRASKPVDGEGDSYLNWYQOKPGKAPKLLIYAASVLES	60
QY	81	GIPDRFSGSGGTDFTLTISRLEPADFAFYICQQSNEDPRTFCQGTRELEIKRTVAAPSVF	140
Db	61	GVPSRFSGSGGTDFTLTISSLQPEDFAFYICQQSHEDPYTFQGTKEIKRTVAAPSVF	120
QY	141	IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS	200
Db	121	IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS	180
QY	201	STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC	238
Db	181	STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC	218

Search completed: April 24, 2002, 15:10:40
Job time: 143 sec

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OM protein - protein search, using sw model

Run on: April 24, 2002, 15:08:22 ; Search time 49.97 Seconds
(without alignments)
362.809 Million cell updates/sec

Title: US-09-499-662-50
Perfect score: 1242
Sequence: 1 METDITLLVLLWVPGSTG.....EVTHQGLSSPVTKSFNRGEC 238

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	984.5	79.3	215	2 JE0242	Ig kappa chain NIG
2	938.5	75.6	215	2 JE0244	Ig kappa chain NIG
3	929.5	74.8	215	2 A23746	Ig kappa chain V-I
4	915.5	73.7	215	2 JE0243	Ig kappa chain NIG
5	885	71.3	216	2 JE0241	Ig kappa chain Am3
6	796	64.1	240	2 S06084	Ig kappa chain pre
7	737	59.3	218	2 S68241	Ig kappa chain V r
8	735	59.2	218	2 JC5810	monoclonal antibod
9	718	57.8	220	2 A31790	Ig kappa chain v r
10	717	57.7	234	2 SI4237	Ig kappa chain pre
11	715.5	57.6	219	2 PC4203	Ig kappa chain (mo
12	715	57.6	210	2 A56169	Ig kappa chain v r
13	713.5	57.4	230	2 S33161	Ig kappa chain - s
14	712.5	57.4	219	2 S52028	Ig kappa chain - m
15	708.5	57.0	219	2 S38865	Ig kappa chain - m
16	703.5	56.6	225	2 S37484	Ig kappa chain - m
17	699.5	56.3	217	2 S42772	Ig kappa chain - m
18	699.5	56.3	219	2 S16112	Ig kappa chain v r
19	688.5	55.4	235	2 S25058	Ig kappa chain - m
20	687	55.3	234	2 S01320	Ig kappa chain pre
21	685.5	55.2	225	2 JL0029	Ig kappa chain pre
22	682	54.9	214	2 S68212	Ig kappa chain (Ma
23	613	49.4	178	2 PT0219	Ig kappa chain V-C
24	609.5	49.1	197	2 S29593	Ig kappa chain (WM
25	602.5	48.5	135	2 S52059	JC-kappa protein -
26	574.5	46.3	229	2 A20969	Ig kappa chain pre
27	571	46.0	131	2 PH1226	Ig kappa chain pre
28	571	46.0	144	2 PL0106	Ig kappa chain pre
29	558.5	45.0	238	2 A49633	Ig lambda-like cha

30	552.5	44.5	145	2 S20631	Ig kappa chain - h
31	548	44.1	106	1 K3HU	Ig kappa chain C r
32	529.5	42.6	129	1 K3HUHA	Ig kappa chain pre
33	527.5	42.5	128	2 S20636	Ig kappa chain V r
34	524.5	42.2	129	2 S49532	Ig kappa chain V r
35	523.5	42.1	129	1 K3HUHI	anti-5m antibody v
36	522	42.0	131	1 KYMSM6	Ig kappa chain pre
37	519.5	41.8	129	2 S46369	Ig light chain var
38	519.5	41.8	134	2 S38643	Ig kappa chain V r
39	513	41.3	99	2 A37927	Ig kappa chain C r
40	508	40.9	132	1 KYMS32	Ig kappa chain pre
41	507	40.8	99	2 S26653	Ig kappa chain C r
42	504.5	40.6	129	2 A32274	Ig kappa chain pre
43	503	40.5	233	2 S29577	Ig light chain - r
44	499	40.2	128	2 A56701	Ig kappa chain V r
45	498	40.1	140	2 PN0446	Ig kappa chain pre

ALIGNMENTS

RESULT 1

JE0242

Ig kappa chain NIG26 precursor - human

C:Species: Homo sapiens (man)

C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JE0242

R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinod

Submitted to JIPID, November 1998

A:Description: Structure relationship of kappatype light chains with AL amyloidosis

A:Reference number: JE0241

A:Accession: JE0242

A:Molecule type: protein

A:Residues: 1-215 <ALI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-91/Domain: immunoglobulin homology <INMS>

Query Match 79.3%; Score 984.5; DB 2; Length 215;
Best Local Similarity 88.1%; Pred. No. 4.2e-59;
Matches 192; Conservative 10; Mismatches 13; Indels 3; Gaps 1;

Qy	21	DIVLTQSPGTLSLSPGERATLSCASQSYVDYDGSYNNMYQKQPGAPRLIYAASNL	80
Db	1	EIVLTQSPGTLSLSPGERATLSCASQSYVDYDGSYNNMYQKQPGAPRLIYAASNL	80
Qy	81	GIPDRFSGSGSTDFTLISRLPEADFAVYVQCSNEDPRTFGQGRLEIKETVAAPSV	140
Db	58	GIPDRFSGSGSTDFTLISRLPEADFAVYVQCSNEDPRTFGQGRLEIKETVAAPSV	117
Qy	141	IFPPSDEQLKSGTASVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSTYSLS	200
Db	118	IFPPSDEQLKSGTASVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSTYSLS	177
Qy	201	STLTLSKADYKHKHYACEVTHQGLSSPVTKSFNRGEC	238
Db	178	STLTLSKADYKHKHYACEVTHQGLSSPVTKSFNRGEC	215

RESULT 2

JE0244

Ig kappa chain NIG2 precursor - human

C:Species: Homo sapiens (man)

C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JE0244

R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H

Submitted to JIPID, November 1998

A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL

A:Reference number: JE0243

A:Accession: JE0244

A:Molecule type: protein

A:Residues: 1-215 <ALI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 75.6%; Score 938.5; DB 2; Length 215;
 Best Local Similarity 84.9%; Pred. No. 5e-56;
 Matches 186; Conservative 10; Mismatches 18; Indels 5; Gaps 2;

QY 21 DIVLTQSPGTLSPGERATLSCAKASQSYVDYDGDSYMNNYQOKPGQAPRLIIYAASNL 80
 :||||| :|||:|||||:||||| : : |||||:|||||:||||| :
 Db 1 EVVLTSQATLSVSPGERATLSCASQSV----HSLAWYQOKPGQAPRLIIYRASTRAT 56
 :||||| :|||:|||||:||||| : : |||||:|||||:||||| :
 QY 81 GIPDRFSGSGGTDTLTISRLEPADFAVYYCQSQNE-DPRTFGQGTREIKRTVAAPSV 139
 :||| :|||:|||||:||||| : |||||:|||||:||||| :
 Db 57 GIPARFSGSGGTDTLTISRLEPADFAVYYCQSQNE-DPRTFGQGTREIKRTVAAPSV 116
 :||| :|||:|||||:||||| : |||||:|||||:||||| :
 QY 140 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 199
 :||| :|||:|||||:||||| : |||||:|||||:||||| :
 Db 117 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 176
 :||| :|||:|||||:||||| : |||||:|||||:||||| :
 QY 200 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 :||| :|||:|||||:||||| : |||||:|||||:||||| :
 Db 177 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215
 :||| :|||:|||||:||||| : |||||:|||||:||||| :

RESULT 3
 A23746
 Ig kappa chain V-III (KAU cold agglutinin) - human
 C:Species: Homo sapiens (man)
 C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
 C:Accession: A23746
 R:Leoni, J.; Ghiso, J.; Coni, F.; Frangione, B.
 J. Biol. Chem. 266, 2836-2842, 1991
 A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin
 A:Reference number: A23746; MUID:91131575
 A:Accession: A23746
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-215 <LEO>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 74.8%; Score 929.5; DB 2; Length 215;
 Best Local Similarity 86.6%; Pred. No. 2e-55;
 Matches 188; Conservative 7; Mismatches 19; Indels 3; Gaps 1;

QY 21 DIVLTQSPGTLSPGERATLSCAKASQSYVDYDGDSYMNNYQOKPGQAPRLIIYAASNL 80
 :||||| :|||:|||||:||||| : : |||||:|||||:||||| :
 Db 1 EIVLTQSPATLSLSPGERATLSCGASQSV---SSNLAWYQOKPGQAPRLIIYDASSRAT 57
 :||||| :|||:|||||:||||| : |||||:|||||:||||| :
 QY 81 GIPDRFSGSGGTDTLTISRLEPADFAVYYCQSQNE-DPRTFGQGTREIKRTVAAPSV 140
 :||||| :|||:|||||:||||| : |||||:|||||:||||| :
 Db 58 GIPDRFSGSGGTDTLTISRLEPADFAVYYCQSQNE-DPRTFGQGTREIKRTVAAPSV 117
 :||||| :|||:|||||:||||| : |||||:|||||:||||| :
 QY 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 200
 :||| :|||:|||||:||||| : |||||:|||||:||||| :
 Db 118 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 177
 :||| :|||:|||||:||||| : |||||:|||||:||||| :
 QY 201 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGE 237
 :||| :|||:|||||:||||| : |||||:|||||:||||| :
 Db 178 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGE 214
 :||| :|||:|||||:||||| : |||||:|||||:||||| :

RESULT 4
 JE0243
 Ig kappa chain NIG93 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
 C:Accession: JE0243
 R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, H.; T.
 submitted to JIPID, November 1998
 A:Description: A new subgroup of k type light chains (Vk) identified in cases of AL amy

A:Reference number: JE0243
 A:Accession: JE0243
 A:Molecule type: protein
 A:Residues: 1-215 <ALI>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 73.7%; Score 915.5; DB 2; Length 215;
 Best Local Similarity 82.6%; Pred. No. 1.7e-54;
 Matches 181; Conservative 14; Mismatches 19; Indels 5; Gaps 2;

QY 21 DIVLTQSPGTLSPGERATLSCAKASQSYVDYDGDSYMNNYQOKPGQAPRLIIYAASNL 80
 :||||| :|||:|||||:||||| : : |||||:|||||:||||| :
 Db 1 EIVLTQSPATLSVSPGERATLSCASQSV----ATNVVYQOKPGQAPRLIIYDASTRAT 56
 :||||| :|||:|||||:||||| : : |||||:|||||:||||| :
 QY 81 GIPDRFSGSGGTDTLTISRLEPADFAVYYCQSQNE-DPRTFGQGTREIKRTVAAPSV 139
 :||| :|||:|||||:||||| : |||||:|||||:||||| :
 Db 57 GVPARFSGSGGTDTLTISRLEPADFAVYYCQSQNE-DPRTFGQGTREIKRTVAAPSV 116
 :||| :|||:|||||:||||| : |||||:|||||:||||| :
 QY 140 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 199
 :||| :|||:|||||:||||| : |||||:|||||:||||| :
 Db 117 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 176
 :||| :|||:|||||:||||| : |||||:|||||:||||| :
 QY 200 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 :||| :|||:|||||:||||| : |||||:|||||:||||| :
 Db 177 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215
 :||| :|||:|||||:||||| : |||||:|||||:||||| :

RESULT 5
 JE0241
 Ig kappa chain Am37 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
 C:Accession: JE0241
 R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda
 submitted to JIPID, November 1998
 A:Description: Structure relationship of kappa type light chains with AL amyloidosis:
 A:Reference number: JE0241
 A:Accession: JE0241
 A:Molecule type: protein
 A:Residues: 1-216 <ALI>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F;16-92/Domain: immunoglobulin homology <IMM>

Query Match 71.3%; Score 885; DB 2; Length 216;
 Best Local Similarity 80.7%; Pred. No. 1.9e-52;
 Matches 176; Conservative 15; Mismatches 25; Indels 2; Gaps 2;

QY 21 DIVLTQSPGTLSPGERATLSCAKASQSYVDYDGDSYMNNYQOKPGQAPRLIIYAASNL 80
 :||||| :|||:|||||:||||| : : |||||:|||||:||||| :
 Db 1 DIVLTQSPDFLAISGERATINCKSSQSVLYNSKNFLAWYQOKPGQ-PKLLIW-ANVRES 58
 :||||| :|||:|||||:||||| : |||||:|||||:||||| :
 QY 81 GIPDRFSGSGGTDTLTISRLEPADFAVYYCQSQNE-DPRTFGQGTREIKRTVAAPSV 140
 :||| :|||:|||||:||||| : |||||:|||||:||||| :
 Db 59 GVPDRFSGSGGTDTLTISRLEPADFAVYYCQSQNE-DPRTFGQGTREIKRTVAAPSV 118
 :||| :|||:|||||:||||| : |||||:|||||:||||| :
 QY 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 200
 :||| :|||:|||||:||||| : |||||:|||||:||||| :
 Db 119 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 178
 :||| :|||:|||||:||||| : |||||:|||||:||||| :
 QY 201 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 :||| :|||:|||||:||||| : |||||:|||||:||||| :
 Db 179 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 216
 :||| :|||:|||||:||||| : |||||:|||||:||||| :

RESULT 6
 S06084
 Ig kappa chain precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
 C:Accession: S06084

A:Description: Isolation and characterisation of sheep kappa light chain cDNA.

A:Reference number: S33161

A:Accession: S33161

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-230 <POL>

A:Cross-references: EMBL:X54110; NID:g297103; PIDN:CAA38046.1; PID:g1364221

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:143-212/Domain: immunoglobulin homology <IMM>

Query Match 57.4%; Score 713.5; DB 2; Length 230;
Best Local Similarity 58.8%; Pred. No. 5.6e-41;
Matches 137; Conservative 37; Mismatches 54; Indels 5; Gaps 2;

QY 7 LLWVLLW-VPGSTGDIVLTQSPGTLSPGERATLSCAKASQSDYDGDYMNWYQOKPG 65

Db 2 LLGULLLWLPGARCDIQVTSFSSLSASLTERVSIICRTSQSV- ---SNLNNWYQOKPG 57

QY 66 QAPRLIIYAASNLESIGIPDFSGSGTDFTLTISRLEPADFAVYVCOQSNEDPRTFGQ 125

Db 58 QAPKLLIYYATRLHTDVPFSGSGTDTLTISNLEANDTATYVCLQYESTPLAEGG 117

QY 126 TRLEIKRTVAAPSVFIPPPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQE 185

Db 118 TNVEIKRSDAQPSVFLFKPSEQLRTGTSVWCLVNDYFYPKIDNVKVDGVTQNSNFQ 177

QY 186 SVTEQDSKSTYSLSSTLTLSKADYKHYACEVTHQGLSSPVTKSFNRGEC 238

Db 178 SFTDQDSKKSTYSLSSTLTLSSEYSHNAYACEVSHKSLPTALVKSFNRNEC 230

RESULT 14

S52028

Ig kappa chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000

C:Accession: S52028

R:Van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schots, A.;

submitted to the EMBL Data Library, August 1994

A:Description: Coordinate expression of antibody subunit genes yields high levels of fun

A:Reference number: S52028

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-219 <VAN>

A:Cross-references: EMBL:L35138; NID:g522336; PIDN:AAA67525.1; PID:g522337

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 57.4%; Score 712.5; DB 2; Length 219;
Best Local Similarity 60.7%; Pred. No. 6.2e-41;
Matches 133; Conservative 36; Mismatches 49; Indels 1; Gaps 1;

QY 21 DIVLTQSPGTLSPGERATLSCAKASQSDYDGDYMNWYQOKPGOAPRLIIYAASNLE 79

Db 1 DVVMTQSPSLPVLGSDQASISCRSQSVHSGNTVLEWYLOKPGQSPKLLIYKVSNR 60

QY 80 SGIPDRFSGSGTDFTLTISRLEPADFAVYVCOQSNEDPRTFGQTRLEIKRTVAAPSV 139

Db 61 SGVPDRFSGSGTDFTLKISRVEAEDLGVIYFCQSHVPTTFGGGTGNTLEIKRAAAPT 120

QY 140 FIPTPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSVTEQDSKSTYS 199

Db 121 SIPTPSEQLTSGASVWVCLNNFYPKIDNVKWKIDGSRQNGVLSWTQDSKSTYS 180

QY 200 SSTLTLSKADYKHYACEVTHQGLSSPVTKSFNRGEC 238

Db 181 SSTLTLTCKDEYERHNSYTCETHKSTSPIVKSFNRNEC 219

RESULT 15

S38865

Ig kappa chain - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar-2001

C:Accession: S38865

R:Kipp, B.; Becker, W.; Schlaak, M.

submitted to the EMBL Data Library, November 1993

A:Description: Combination of a defined specificity and desired isotype by cloning o

A:Reference number: S38864

A:Accession: S38865

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-219 <KIP>

A:Cross-references: EMBL:227396; NID:g416538; PIDN:CAA81787.1; PID:g416539

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 57.0%; Score 708.5; DB 2; Length 219;
Best Local Similarity 60.7%; Pred. No. 1.1e-40;
Matches 133; Conservative 37; Mismatches 48; Indels 1; Gaps 1;

QY 21 DIVLTQSPGTLSPGERATLSCAKASQSDYDGDSTMNWYQOKPGOAPRLIIYAASNLE 79

Db 1 ELVMTQSPSLSVSLGSDQASISCRSQSLVHTNGNTVLEWYLOKPGSLPKLLIYIVSNRF 60

QY 80 SGIPDRFSGSGTDFTLTISRLEPADFAVYVCOQSNEDPRTFGQTRLEIKRTVAAPSV 139

Db 61 SGVPDRFSGSGTDFTLKISRVEAEDLGVIYFCQSHVPTTFGGGTGNTLEIKRAAAPT 120

QY 140 FIPTPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSVTEQDSKSTYS 199

Db 121 SIPTPSEQLTSGASVWVCLNNFYPKIDNVKWKIDGSRQNGVLSWTQDSKSTYS 180

QY 200 SSTLTLSKADYKHYACEVTHQGLSSPVTKSFNRGEC 238

Db 181 SSTLTLTCKDEYERHNSYTCETHKSTSPIVKSFNRGEC 219

Search completed: April 24, 2002, 15:11:36

Job time: 194 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 15:08:23 ; Search time 29.21 Seconds
(without alignments)
298.741 Million cell updates/sec

Title: US-09-499-662-50

Perfect score: 1242

Sequence: 1 METDTILLVLLWVPSTG.....EVTHQGLSSPVTKSFNRGEC 238

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	548	44.1	106	1	KAC_HUMAN	P01834 homo sapien
2	529.5	42.6	129	1	KV3L_HUMAN	P18135 homo sapien
3	523.5	42.1	129	1	KV3M_HUMAN	P18136 homo sapien
4	522	42.0	131	1	KV3I_MOUSE	P01661 mus musculus
5	508	40.9	132	1	KV3F_MOUSE	P01658 mus musculus
6	482	38.8	128	1	KV3C_HUMAN	P06311 homo sapien
7	473	38.1	111	1	KV3M_MOUSE	P01665 mus musculus
8	471	37.9	111	1	KV3M_MOUSE	P01666 mus musculus
9	469	37.8	111	1	KV3O_MOUSE	P01667 mus musculus
10	466	37.5	111	1	KV3Q_MOUSE	P01669 mus musculus
11	462.5	37.2	129	1	KV3H_HUMAN	P04207 homo sapien
12	459.5	37.0	109	1	KV3B_HUMAN	P01620 homo sapien
13	458	36.9	111	1	KV3L_MOUSE	P01664 mus musculus
14	456.5	36.8	109	1	KV3D_HUMAN	P01622 homo sapien
15	452.5	36.4	109	1	KV3E_HUMAN	P01623 homo sapien
16	448.5	36.1	110	1	KV3P_MOUSE	P01668 mus musculus
17	446	35.9	115	1	KV3I_HUMAN	P04333 homo sapien
18	437	35.2	134	1	KV4C_HUMAN	P06314 homo sapien
19	435.5	35.1	109	1	KV3G_HUMAN	P04206 homo sapien
20	428.5	34.5	133	1	KV2F_HUMAN	P06310 homo sapien
21	428	34.5	111	1	KV3H_MOUSE	P01660 mus musculus
22	424.5	34.2	108	1	KV3A_HUMAN	P01619 homo sapien
23	423	34.1	129	1	KV1W_HUMAN	P04431 homo sapien
24	421.5	33.9	133	1	KV4B_HUMAN	P06313 homo sapien
25	420.5	33.9	116	1	KV3J_MOUSE	P04434 homo sapien
26	417	33.6	111	1	KV3J_MOUSE	P01662 mus musculus
27	416	33.5	111	1	KV3K_MOUSE	P01663 mus musculus
28	410	33.0	111	1	KV3R_MOUSE	P01670 mus musculus
29	405.5	32.6	109	1	KV3F_HUMAN	P01624 homo sapien
30	403	32.4	114	1	KV4A_HUMAN	P01625 homo sapien
31	402	32.4	111	1	KV3S_MOUSE	P01671 mus musculus
32	402	32.4	112	1	KV3G_MOUSE	P01659 mus musculus
33	401	32.3	108	1	KV1H_HUMAN	P01600 homo sapien

RESULT 1

ID	KAC_HUMAN	STANDARD	PRT	106 AA
AC	P01834			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	IG KAPPA CHAIN C REGION			
GN	IGKC			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE (MYELOMA PROTEIN EU)			
RX	MEDLINE=71064023; PubMed=5489770;			
RA	Gotlib P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain."			
RL	Biochemistry 9:3155-3161(1970).			
RN	[2]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds."			
RL	Biochemistry 9:3188-3196(1970).			
RN	[3]			
RP	SEQUENCE (BENCE-JONES PROTEIN TI)			
RX	MEDLINE=72188439; PubMed=5027703;			
RA	Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;			
RT	"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81042304; PubMed=6775818;			
RA	Hietter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;			
RT	"Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments."			
RL	Cell 22:197-207(1980).			
RN	[5]			
RP	SEQUENCE (BENCE-JONES PROTEIN ROY)			
RA	Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,			
RT	Steinmetz-Kayne M., Suter L., Watanabe S.;			
RL	(In) Franek F., Shugar D. (eds.);			
RN	Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).			
RP	[6]			
RX	SEQUENCE (BENCE-JONES PROTEIN CUM)			
RL	MEDLINE=68242259; PubMed=5586923;			
RA	Hilschmann N.;			
RT	"The complete amino acid sequence of Bence Jones protein Cum (kappa-type)."			

34	401	32.3	111	1	KV3U_MOUSE	P01673 mus musculus
35	400.5	32.2	100	1	KV3C_HUMAN	P01621 homo sapien
36	397	32.0	108	1	KV1K_HUMAN	P01603 homo sapien
37	397	32.0	111	1	KV3C_MOUSE	P01656 mus musculus
38	396	31.9	108	1	KV1N_HUMAN	P01606 homo sapien
39	396	31.9	111	1	KV3T_MOUSE	P01672 mus musculus
40	394	31.7	111	1	KV2D_HUMAN	P01654 mus musculus
41	391.5	31.5	113	1	KV2D_HUMAN	P01617 homo sapien
42	390	31.4	108	1	KV1M_HUMAN	P01605 homo sapien
43	388.5	31.3	117	1	KV2E_HUMAN	P06309 homo sapien
44	387	31.2	117	1	KV1J_HUMAN	P01602 homo sapien
45	386.5	31.1	112	1	KV3B_MOUSE	P01655 mus musculus

ALIGNMENTS

RL Hoppe-Seyler's 2. Physiol. Chem. 348:1718-1722(1967).
 [17]
 RN SEQUENCE (BENCE-JONES PROTEIN AG).
 RX MEDLINE=69234734; PubMed=4893682;
 RA Titani K., Shinoda T., Putnam F.W.;
 RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
 complete sequence and the location of the disulfide bridges.";
 RL J. Biol. Chem. 244:3550-3560(1969).
 RN [8]
 RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
 RX MEDLINE=70201507; PubMed=5447531;
 RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
 RT "Macroglobulin structure: variable sequence of light and heavy
 chains.";
 RL Science 169:56-59(1970).
 CC -!- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
 CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
 CC MARKER, 45-ALA AND 83-LEU.
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 DR EMBL: J00241; AAA58989.1; -;
 DR EMBL: V00557; CAA23823.1; -;
 DR PIR: A02116; K3HU.
 DR MIM: 147200; -;
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_c1.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00407; Igc1; 1.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DISULFID 26 86
 FT DISULFID 106 106
 FT VARIANT 83 83
 FT INTERCHAIN (WITH A HEAVY CHAIN).
 FT D -> L (IN INV(1,2) MARKER).
 FT /FTID=VAR_003897.
 FT E -> N (IN REF. 7 AND 8).
 FT E -> Q (IN REF. 5 AND 6).
 FT CONFLICT 14 14
 FT CONFLICT 57 57
 FT SEQUENCE 106 AA; 11609 MW; 51984D1FDD372CE8 CRC64;
 SQ

Query Match 44.13; Score 548; DB 1; Length 106;
 Best Local Similarity 100.0%; Pred. No. 6.2e-39;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 133 TVAAPSVFIFFPSDQLSGTASVVCLLNFPYKQVQKVDNALQSGNSQESVTEQDS 192
 Db 1 TVAAPSVFIFFPSDQLSGTASVVCLLNFPYKQVQKVDNALQSGNSQESVTEQDS 60
 QY 193 KDSYSLSTLTSLKADYEKIKVYACEVTHOGLSPVTKSFNRGEC 238
 Db 61 KDSYSLSTLTSLKADYEKIKVYACEVTHOGLSPVTKSFNRGEC 106
 RESULT 2
 ID KV3L_HUMAN STANDARD; PRT; 129 AA.
 AC P18135;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION HAH PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=88171307; PubMed=3127527;
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
 RT "Autoantibody-associated kappa light chain variable region gene
 expressed in chronic lymphocytic leukemia with little or no somatic
 mutation. Implications for etiology and immunotherapy.";
 RL J. Exp. Med. 167:840-852(1988).
 CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
 CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
 CC LEUKEMIA.
 DR PIR: P18135; K3HUHA.
 DR HSSP: P01789; 2MCP.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; Igv; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 56 70 FRAMEWORK 2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 78 109 FRAMEWORK 3.
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 119 129 JK1 SEGMENT.
 FT DISULFID 43 109 BY SIMILARITY.
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;
 Query Match 42.68; Score 529.5; DB 1; Length 129;
 Best Local Similarity 78.08; Pred. No. 2.7e-37;
 Matches 103; Conservative 11; Mismatches 15; Indels 3; Gaps 1;
 QY 1 METDTILLWVLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCAKASQVVDYDGDSYMMNY 60
 Db 1 METPAQLLFLLELLWLPDPTGEIVLTQSPGTLSLSPGERATLSCRAQSV--SSSYLAWY 57
 QY 61 QOKPGQAPRLIIYAASNLKESGIPDRFSGSGSGTDFTLTISRLEPADFAVYVCOQSNEDPR 120
 Db 58 QOKPGQAPRLIIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPADFAVYVCOQGTSPR 117
 QY 121 TFGQGTREIKR 132
 Db 118 TFGQGTREIKR 129
 RESULT 3
 ID KV3M_HUMAN STANDARD; PRT; 129 AA.
 AC P18136;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION HIC PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88171307; PubMed=3127527;
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
 RT "Autoantibody-associated kappa light chain variable region gene
 expressed in chronic lymphocytic leukemia with little or no somatic
 mutation. Implications for etiology and immunotherapy.";
 RL J. Exp. Med. 167:840-852(1988).
 CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
 CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
 CC LEUKEMIA.
 DR PIR: P18135; K3HUHI.
 DR HSSP: P01789; 2MCP.

```
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_v.
DR SMART: SM00406; IGV: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
FT SEQUENCE 129 AA; 7395528EA2BB74D6 CRC64;

Query Match 42.1%; Score 523.5; DB 1; Length 129;
Best Local Similarity 77.3%; Pred. No. 8.5e-37;
Matches 102; Conservative 11; Mismatches 16; Indels 3; Gaps 1;

QY 1 METDTILLWLLVPGSTGDIVLTQSPGTLSLSPGERATLSCASQSYVDGDSYNNWY 60
DB 1 METPAQLFLLLWLPDTTGEIVLTQSPGTLSLSPGERATLSCASQSV---SSSYLAWY 57
QY 61 QOKPGQAPRLIIAASNLGSGIPDRFSGSGGTDFLTISRLEPADFAVYYCOOSNEDPR 120
DB 58 QOKPGQAPRLIIVGASRATGIPDRFSGSGGTDFLTISRLEPADFAVYYCOOYGSSPW 117
QY 121 TFGQGTREIKR 132
DB 118 TFGQGTREIKR 129

RESULT 4
KV3I_MOUSE
ID KV3I_MOUSE STANDARD; PRT; 131 AA.
AC P01661;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION MOPC 63 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-35.
RX MEDLINE=78235887; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes.";
RL Biochemistry 17:2392-2400(1978).
RN [2]
RP SEQUENCE OF 21-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences.";
RL Biochemistry 12:760-771(1973).
RN [3]
RP REVISIONS.
RX McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
DR PIR: A01935; KVM5M6.
DR InterPro: IPR003006; Ig_MHC.
```

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DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 131
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 59 73 FRAMEWORK 2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 81 112 FRAMEWORK 3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 122 131 FRAMEWORK 4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON_TER 131 131
FT SEQUENCE 131 AA; D212EC9F08DC880A CRC64;

Query Match 42.0%; Score 522; DB 1; Length 131;
Best Local Similarity 74.8%; Pred. No. 1.2e-36;
Matches 98; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

QY 1 METDTILLWLLVPGSTGDIVLTQSPGTLSLSPGERATLSCASQSYVDGDSYNNWY 60
DB 1 METDTLLWLLVPGSTGDIVLTQSPGTLSLSPGERATLSCASQSYVDGDSYNNWY 60
QY 61 QOKPGQAPRLIIAASNLGSGIPDRFSGSGGTDFLTISRLEPADFAVYYCOOSNEDPR 120
DB 61 QOKPGQAPRLIIVLASNLGSGIPDRFSGSGGTDFLTISRLEPADFAVYYCOONEDPW 120
QY 121 TFGQGTREIKR 131
DB 121 TFGQGTREIKR 131

RESULT 5
KV3F_MOUSE
ID KV3F_MOUSE STANDARD; PRT; 132 AA.
AC P01658;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION MOPC 321 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-37.
RX MEDLINE=78235887; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes.";
RL Biochemistry 17:2392-2400(1978).
RN [2]
RP SEQUENCE OF 21-132.
RX MEDLINE=73140224; PubMed=4120629;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Partial amino acid sequence of a kappa
RT chain.";
RL Biochemistry 12:749-759(1973).
CC -1- MISCELLANEOUS: THE PARTIAL SEQUENCE OF THE C REGION OF THIS
CC BENCE-JONES PROTEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT
CC REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY
CC RESIDUES.
DR PIR: A01933; KVM532.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV: 1.
KW Immunoglobulin V region; Bence-Jones protein; Signal.
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FT SIGNAL 1 20
FT CHAIN 21 132
FT DOMAIN 21 43
FT DOMAIN 21 43
FT DOMAIN 44 58
FT DOMAIN 59 73
FT DOMAIN 74 80
FT DOMAIN 81 112
FT DOMAIN 113 121
FT DOMAIN 122 131
FT DISULFID 42 112
FT NON_TER 132 132
SQ SEQUENCE 132 AA; 14523 MW; 9F3B809BB773FBE9 CRC64;

Query Match 40.98; Score 508; DB 1; Length 132;
Best Local Similarity 67.48; Pred. No. 1.7e-35;
Matches 89; Conservative 26; Mismatches 17; Indels 0; Gaps 0;

Qy 1 METDTLLVLLWVPGSTGDIVLTQSPGTLSPGERATLSCASQSDVDGDSYNNWY 60
Db 1 METDTLLVLLWVPGSTGDIVLTQSPASLAVSLGQRTATISCRASKSVNTYGNFHWY 60

Qy 61 QOKPGQAPRLIYAASNLSEGIPIRFGSGSGDTFTLTISRLPADFAVYCCQSNEDPR 120
Db 61 ZKPGZPPKLLIYRASNLSGIPARFSGSGRTFTLTIBPVZABDVATYPCZZSBZBPW 120

Qy 121 TFGGTRLEIKR 132
Db 121 TFGGTRLEIKR 132

RESULT 6
KV3M_HUMAN STANDARD; PRT; 128 AA.
ID KV3M_HUMAN
AC P06311;
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION IARC/BL41 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobbeck H.G., Meindl A., Combrato G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and III.";
RL Nucleic Acids Res. 13:6499-6513(1985).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; Z00021; CAA77316.1; -
DR PIR; A01899; K3HU41.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
KV SIGNAL 1 20
FT CHAIN 21 128
FT DOMAIN 21 43
FT DOMAIN 44 54
FT DOMAIN 55 69
FT DOMAIN 70 76
FT DOMAIN 77 108

IG KAPPA CHAIN V-III REGION IARC/BL41.
FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2.
FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING 3.
FRAMEWORK 4.
COMPLEMENTARITY-DETERMINING 4.
BY SIMILARITY.

Query Match 40.98; Score 508; DB 1; Length 132;
Best Local Similarity 67.48; Pred. No. 1.7e-35;
Matches 89; Conservative 26; Mismatches 17; Indels 0; Gaps 0;
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FT DOMAIN 109 117
FT DOMAIN 118 128
FT DISULFID 43 108
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;

Query Match 38.88; Score 482; DB 1; Length 128;
Best Local Similarity 73.58; Pred. No. 2.3e-33;
Matches 97; Conservative 12; Mismatches 19; Indels 4; Gaps 1;

Qy 1 METDTLLVLLWVPGSTGDIVLTQSPGTLSPGERATLSCASQSDVDGDSYNNWY 60
Db 1 METDTLLVLLWVPGSTGDIVLTQSPGTLSPGERATLSCASQSDVDGDSYNNWY 60

Qy 61 QOKPGQAPRLIYAASNLSEGIPIRFGSGSGDTFTLTISRLPADFAVYCCQSNEDPR 120
Db 61 ZKPGZPPKLLIYRASNLSGIPARFSGSGRTFTLTIBPVZABDVATYPCZZSBZBPW 120

Qy 121 TFGGTRLEIKR 132
Db 121 TFGGTRLEIKR 128

RESULT 7
KV3M_MOUSE STANDARD; PRT; 111 AA.
ID KV3M_MOUSE
AC P01665;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7043.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gammaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin diversity.";
RL Nature 276:785-790(1978)
DR PIR; A01937; KVS43;
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
KV DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 61
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 7A5FCB586C306D29 CRC64;

Query Match 38.18; Score 473; DB 1; Length 111;
Best Local Similarity 81.18; Pred. No. 1.1e-32;
Matches 90; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

Qy 21 DIVLTQSPGTLSPGERATLSCASQSDVDGDSYNNWYQOKPGQAPRLIYAASNLSE 80
Db 1 DIVLTQSPASLAVSLGQRTATISCRASKSVNTYGNFHWY 60

Qy 81 GIPDRFSGSGSGDTFTLTISRLPADFAVYCCQSNEDPRFTFGGTRLEIK 131
Db 61 GIPARFSGSGSGDTFTLTINHPVEEDAATYCCQSNEDPFTFGGTRLEIK 111
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FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111
SQ SEQUENCE 111 AA; 11964 MW; E2B1AD98AD965962 CRC64;

Query Match 36.9%; Score 458; DB 1; Length 111;
Best Local Similarity 78.4%; Pred. No. 1.8e-31;
Matches 87; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

Qy 21 DIVLTQSPGTLSPGERATLSCRASQSVVDGDSYMNWYQKPGQAPRLIIYAASNLES 80
Db 1 DIVLTQSPGTLSPGERATLSCRASQSVVDGDSYMNWYQKPGQAPRLIIYAASNLES 60

Qy 81 GIPDRFSGSGGTDFTLISRLPEADFAVYVYQSQSNEDPRFTFGQTRLEIK 131
Db 61 GIPARFSGSGGTDFTLNHPVEEDAATYVYQSQSNEDPYTFGGTKLEIK 111

RESULT 14
KV3D_HUMAN
ID KV3D_HUMAN STANDARD; PRT; 109 AA.
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION TI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human Igm anti-gamma-globulins of the Wa
RT group.";
RL Biochemistry 20:5816-5822(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01896; K3HUTL.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR003596; Iq_V.
DR Pfam; PF00047; Iq; 1.
DR SMART; SM00406; Iq; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11746 MW; 566C115E6B9CBEE CRC64;

Query Match 36.4%; Score 452.5; DB 1; Length 109;
Best Local Similarity 79.5%; Pred. No. 5.2e-31;
Matches 89; Conservative 7; Mismatches 13; Indels 3; Gaps 1;

Qy 21 DIVLTQSPGTLSPGERATLSCRASQSVVDGDSYMNWYQKPGQAPRLIIYAASNLES 80
Db 1 EIVLTQSPGTLSPGERATLSCRASQSV---SSGYLGWYQKPGQAPRLIIYGASSRAT 57

Qy 81 GIPDRFSGSGGTDFTLISRLPEADFAVYVYQSQSNEDPRFTFGQTRLEIKR 132
Db 58 GIPDRFSGSGGTDFTLISRLPEADFAVYVYQSQYGLGRFTFGQTKVEIKR 109

Search completed: April 24, 2002, 15:13:45
Job time: 322 sec
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FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111
SQ SEQUENCE 111 AA; 11964 MW; E2B1AD98AD965962 CRC64;

Query Match 36.9%; Score 458; DB 1; Length 111;
Best Local Similarity 78.4%; Pred. No. 1.8e-31;
Matches 87; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

Qy 21 DIVLTQSPGTLSPGERATLSCRASQSVVDGDSYMNWYQKPGQAPRLIIYAASNLES 80
Db 1 DIVLTQSPGTLSPGERATLSCRASQSVVDGDSYMNWYQKPGQAPRLIIYAASNLES 60

Qy 81 GIPDRFSGSGGTDFTLISRLPEADFAVYVYQSQSNEDPRFTFGQTRLEIK 131
Db 61 GIPARFSGSGGTDFTLNHPVEEDAATYVYQSQSNEDPYTFGGTKLEIK 111

RESULT 14
KV3D_HUMAN
ID KV3D_HUMAN STANDARD; PRT; 109 AA.
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION TI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT Ti). IV. The complete amino acid sequence and its significance for
RT the mechanism of antibody production.";
RL Hoppe-Sevler's Z. Physiol. Chem. 353:189-208(1972).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
DR PIR; A01895; K3HUTI.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR003596; Iq_V.
DR Pfam; PF00047; Iq; 1.
DR SMART; SM00406; Iq; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;

Query Match 36.8%; Score 456.5; DB 1; Length 109;
Best Local Similarity 78.6%; Pred. No. 2.4e-31;
Matches 88; Conservative 10; Mismatches 11; Indels 3; Gaps 1;

Qy 21 DIVLTQSPGTLSPGERATLSCRASQSVVDGDSYMNWYQKPGQAPRLIIYAASNLES 80
Db 1 EIVLTQSPGTLSPGERATLSCRASQSV---SNSFLAWYQKPGQAPRLIIYVASSRAT 57

Qy 81 GIPDRFSGSGGTDFTLISRLPEADFAVYVYQSQSNEDPRFTFGQTRLEIKR 132
Db 58 GIPDRFSGSGGTDFTLISRLPEADFAVYVYQSQYGLGRFTFGQTKVELKR 109
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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	752.5	60.6	238	11	Q99W37	Q99m37 mus musculus
2	686	55.2	214	11	Q9RIA5	Q9rla5 mus musculus
3	445.5	35.9	109	4	Q9UL78	Q9ul78 homo sapien
4	422.5	34.0	109	4	Q9UL86	Q9ul86 homo sapien
5	419.5	33.8	235	11	Q99W11	Q99m11 mus musculus
6	405	32.6	108	4	Q9UL77	Q9ul77 homo sapien
7	394	31.7	108	4	Q9UL83	Q9ul83 homo sapien
8	389	31.3	108	4	Q9UL79	Q9ul79 homo sapien
9	387	31.2	108	4	Q9UL70	Q9ul70 homo sapien
10	385.5	31.0	109	4	Q9UL85	Q9ul85 homo sapien
11	375.5	30.2	107	4	Q9UL81	Q9ul81 homo sapien
12	363	29.2	103	11	Q9JL80	Q9j180 mus musculus
13	362	29.1	114	4	Q9UL80	Q9ul80 homo sapien
14	345.5	27.8	106	5	Q9U410	Q9u410 schistosoma
15	331	26.7	298	11	Q9QYF0	Q9qyf0 mus musculus
16	330	26.6	109	11	Q9UL74	Q9j174 mus musculus
17	330	26.6	107	11	Q9ERZ9	Q9erz9 mus musculus
18	329.5	26.5	104	11	Q9JL82	Q9j182 mus musculus
19	319	25.7	197	11	Q9JL76	Q9j176 mus musculus

```
RESULT 2
Q9RIA5 PRELIMINARY; PRT; 214 AA.
AC Q9RIA5:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RZ SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Mista S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF152371; AAD40242.1; -.
DR HSP; P01789; IMCP.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 55.2%; Score 686; DB 11; Length 214;
Best Local Similarity 58.7%; Pred. No. 7e-56;
Matches 128; Conservative 34; Mismatches 52; Indels 4; Gaps 1;

Qy 21 DIVLTQSPGCTLSLSPGERATLSCASQSVYDGDSDYNNYQOKPGQAPRLIIYAASNL 80
Db 1 DIVLTQSPSSVYASIGERVTITCKASQDI---NSILSWFOQKPGKSPKTLIYRANRLVD 56

Qy 81 GIPDRFSGSGGTDFLTISRLEPAFAVYVYQQSNEDPRTFGQTRLEIKRVAAPSVF 140
Db 57 GVPSRFSGSGQQDYLISLSEYEDMGIIYCYQVDEFFTFGSGTKLEIKRADAPVVS 116

Qy 141 IFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 200
Db 117 IFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 176

Qy 201 STLTLSKADYEKKHYACEVTHOGLSSPVTKSFNRGEC 238
Db 177 STLTLTQDEYERHNSYTCETATHKTSPIVRCFNRNEC 214

RESULT 3
Q9UL78 PRELIMINARY; PRT; 109 AA.
AC Q9UL78:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RZ SEQUENCE FROM N.A.
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035028; AAD56264.1; -.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7D8C83 CRC64;

Query Match 34.0%; Score 422.5; DB 4; Length 109;
Best Local Similarity 75.0%; Pred. No. 8.2e-32;
Matches 84; Conservative 8; Mismatches 17; Indels 3; Gaps 1;

Qy 21 DIVLTQSPGCTLSLSPGERATLSCASQSVYDGDSDYNNYQOKPGQAPRLIIYAASNL 80
Db 1 EIVLTQSPGCTLSLSPGERATLSCASQSV---SSSYLANVYQKPGQAPRLIIYGTSSRAT 57

Qy 81 GIPDRFSGSGGTDFLTISRLEPAFAVYVYQQSNEDPRTFGQTRLEIKR 132
Db 58 GIPDRFSGSGGTDFLTISRLEPAFAVYVYQQSNEDPRTFGQTRLEIKR 109
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RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035036; AAD56272.1; -.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 35.9%; Score 445.5; DB 4; Length 109;
Best Local Similarity 78.6%; Pred. No. 6e-34;
Matches 88; Conservative 7; Mismatches 14; Indels 3; Gaps 1;

Qy 21 DIVLTQSPGCTLSLSPGERATLSCASQSVYDGDSDYNNYQOKPGQAPRLIIYAASNL 80
Db 1 EIVLTQSPGCTLSLSPGERATLSCASQSV---SSSYLANVYQKPGQAPRLIIYGTSSRAT 57

Qy 81 GIPDRFSGSGGTDFLTISRLEPAFAVYVYQQSNEDPRTFGQTRLEIKR 132
Db 58 GIPDRFSGSGGTDFLTISRLEPAFAVYVYQQSNEDPRTFGQTRLEIKR 109

RESULT 4
Q9UL86 PRELIMINARY; PRT; 109 AA.
AC Q9UL86:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RZ SEQUENCE FROM N.A.
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.;
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035028; AAD56264.1; -.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7D8C83 CRC64;

Query Match 34.0%; Score 422.5; DB 4; Length 109;
Best Local Similarity 75.0%; Pred. No. 8.2e-32;
Matches 84; Conservative 8; Mismatches 17; Indels 3; Gaps 1;

Qy 21 DIVLTQSPGCTLSLSPGERATLSCASQSVYDGDSDYNNYQOKPGQAPRLIIYAASNL 80
Db 1 EIVLTQSPGCTLSLSPGERATLSCASQSV---SSSYLANVYQKPGQAPRLIIYGTSSRAT 57

Qy 81 GIPDRFSGSGGTDFLTISRLEPAFAVYVYQQSNEDPRTFGQTRLEIKR 132
Db 58 GIPDRFSGSGGTDFLTISRLEPAFAVYVYQQSNEDPRTFGQTRLEIKR 109
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RESULT 5
Q99M11 ID Q99M11 PRELIMINARY; PRT; 235 AA.
AC Q99M11;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:6743).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003129; AAH0129.1; -.
SQ SEQUENCE 235 AA; 25403 MW; 39807BFE6782A3FB CRC64;

Query Match 33.8%; Score 419.5; DB 11; Length 235;
Best Local Similarity 42.2%; Pred. No. 4.1e-31;
Matches 100; Conservative 36; Mismatches 88; Indels 13; Gaps 7;

QY 7 LLVLLWVPSTGDIVLTQSPGTLSPGERATLSCASQSDYDGSYNNWYQKPGQ 66
Db 6 LLVFLHLLTGSCAQLVLTQ-PSVSSTLSGLSTAKLPCKA--STGNIGDSVNNWYQYMGR 62

QY 67 APRLIYAASNLSEIDPFRSGS--GGTDTFTLISRLPADFAVYVCQSNEDPRTFGQ 124
Db 63 SPTNMIYGDRLRSGVSDRSGSIDSSNSAFLTIQNVQADDEADYVCQSYSSGIRVFGG 122

QY 125 GTRLEI-KRTVAAPSFIFPPSDEQLKGTASVCLLNINFPREAKVQWKNALQSGNS 183
Db 123 GKTALVLSQPKTSPVTLFPSPSEETLNKATLVCTISDFYGVVTVYDWRKADG---TPVT 179

QY 184 QESVTEQDSK--DSTYSLSLTLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 180 QGVETTPQSKNNKYNWASSYLTLTAKAWETHSSYSCQVTHEG--HTVKSLSRADC 234

RESULT 6
Q9UL77 ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035037; AAD56273.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 31.7%; Score 394; DB 4; Length 108;
Best Local Similarity 70.5%; Pred. No. 3.5e-29;
Matches 79; Conservative 11; Mismatches 18; Indels 4; Gaps 1;

QY 21 DIVLTQSPGTLSPGERATLSCASQSDYDGSYNNWYQKPGQAPRLIYAASNL 80
Db 1 EIVMTQSPATILSVSPGERATLSCASQSV-----SSNLAWYQKPGQAPRLIYCASTRAT 56

QY 81 GIPDRFSGSGGTFTLTISRLEPADFAVYVCQSNEDPRTFGQTRLEIKR 132
Db 57 GIPARFSGSGGTFTLTISRLEPADFAVYVCQSNEDPRTFGQTRLEIKR 108

RESULT 8
Q9UL79 ID Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 32.6%; Score 405; DB 4; Length 108;
Best Local Similarity 67.9%; Pred. No. 3.4e-30;
Matches 76; Conservative 16; Mismatches 16; Indels 4; Gaps 1;

QY 21 DIVLTQSPGTLSPGERATLSCASQSDYDGSYNNWYQKPGQAPRLIYAASNL 80
Db 1 DIQMTQSPSSLSASVGDRVTITCRASQSI-----SSYLNWYQKPGKAPNLLIYAASSLQS 56

QY 81 GIPDRFSGSGGTFTLTISRLEPADFAVYVCQSNEDPRTFGQTRLEIKR 132
Db 57 GVPFRFSGSGGTFTLTISRLEPADFAVYVCQSNEDPRTFGQTRLEIKR 108

RESULT 7
Q9UL83 ID Q9UL83 PRELIMINARY; PRT; 108 AA.
AC Q9UL83;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035037; AAD56267.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 31.7%; Score 394; DB 4; Length 108;
Best Local Similarity 70.5%; Pred. No. 3.5e-29;
Matches 79; Conservative 11; Mismatches 18; Indels 4; Gaps 1;

QY 21 DIVLTQSPGTLSPGERATLSCASQSDYDGSYNNWYQKPGQAPRLIYAASNL 80
Db 1 EIVMTQSPATILSVSPGERATLSCASQSV-----SSNLAWYQKPGQAPRLIYCASTRAT 56

QY 81 GIPDRFSGSGGTFTLTISRLEPADFAVYVCQSNEDPRTFGQTRLEIKR 132
Db 57 GIPARFSGSGGTFTLTISRLEPADFAVYVCQSNEDPRTFGQTRLEIKR 108

RESULT 8
Q9UL79 ID Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RT Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035035; AAD56271.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 31.3%; Score 389; DB 4; Length 108;
Best Local Similarity 67.0%; Pred. No. 1e-28;
Matches 75; Conservative 12; Mismatches 21; Indels 4; Gaps 1;

Qy 21 DIVLTQSPGTLSPGERATLSCASQSDVDGDSYMNWYQKPGQAPRLIIYAASNL 80
Db 1 DIVMTQSPATLSVSPGERATLSCASQSI-----SSNLAWYQKPGQAPRLIIYAAS 56

Qy 81 GIPDRFSGSGGTDFTLISRLPADFAVYVYCOOSNEDPRTFGGTRLEIKR 132
Db 57 GVPFRSGSGGTDFTLISRLPADFAVYVYCOOSNEDPRTFGGTRLEIKR 108

Qy 81 GIPDRFSGSGGTDFTLISRLPADFAVYVYCOOSNEDPRTFGGTRLEIKR 132
Db 57 GVPFRSGSGGTDFTLISRLPADFAVYVYCOOSNEDPRTFGGTRLEIKR 108

RESULT 9
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RT Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035029; AAD56265.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;

Query Match 31.0%; Score 385.5; DB 4; Length 109;
Best Local Similarity 69.0%; Pred. No. 2.2e-28;
Matches 78; Conservative 12; Mismatches 18; Indels 5; Gaps 2;

Qy 21 DIVLTQSPGTLSPGERATLSCASQSDVDGDSYMNWYQKPGQAPRLIIYAASNL 80
Db 1 EIVMTQSPATLSVSPGERATLSCASQSI-----SSNLAWYQKPGQAPRLIIYGASTRAT 56

Qy 81 GIPDRFSGSGGTDFTLISRLPADFAVYVYCOOSNEDPRTFGGTRLEIKR 132
Db 57 GIPARFSGSGGTDFTLISRLPADFAVYVYCOOSNEDPRTFGGTRLEIKR 109

RESULT 11
Q9UL81 PRELIMINARY; PRT; 107 AA.
ID Q9UL81
AC Q9UL81;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RT Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035044; AAD56280.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 31.2%; Score 387; DB 4; Length 108;
Best Local Similarity 64.3%; Pred. No. 1.6e-28;
Matches 72; Conservative 16; Mismatches 20; Indels 4; Gaps 1;

Qy 21 DIVLTQSPGTLSPGERATLSCASQSDVDGDSYMNWYQKPGQAPRLIIYAASNL 80

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RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035033; AAD56269.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 107
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 30.2%; Score 375.5; DB 4; Length 107;
Best Local Similarity 64.3%; Pred. No. 1.8e-27;
Matches 72; Conservative 18; Mismatches 17; Indels 5; Gaps 2;

QY 21 DIVLTQSPGTLSPGERATLSCAKSQSDYDGDSTVMNYYQKPGQAPRLIIYAASNL 80
DB 1 DIQMTQSPSSLSASVGRVTITCRASQSI----SNVLNYYQKPGKAPNLLIYAASLS 56

QY 81 GIPDRFSGSGGTDFLTISRLPEADFAVYVYCOQSNEDPTFGQGRLEIKR 132
DB 57 GVPDRFSGSGGTDFLTISGLQAEAFYVYCOQS-YSALTFGPGTKVDLR 107

RESULT 12
Q9UL80 PRELIMINARY; PRT; 103 AA.
AC Q9UL80;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Markiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RT Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF206026; AAF69324.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 103
FT NON_TER 103
SQ SEQUENCE 103 AA; 11224 MW; EC87D653DB3AAB21 CRC64;

Query Match 29.2%; Score 363; DB 11; Length 103;
Best Local Similarity 66.7%; Pred. No. 2.5e-26;
Matches 68; Conservative 17; Mismatches 17; Indels 0; Gaps 0;

QY 30 TLSLSPGERATLSCAKSQSDYDGDSTVMNYYQKPGQAPRLIIYAASNLGIPDRFSGS 89
DB 2 SLAVSLGQRATISCRASEVETGTSIMQVYQKPGQAPRLIIYAASNVESGVPAFSGS 61

QY 90 GSGTDFLTISRLEPADFAVYVYCOQSNEDPTFGQGRLEIKR 131
DB 62 GSGTDFSLNIHPVEDDIAMVFCQSKRPVWTFGGTGKLEIK 103

RESULT 13
Q9UL80 PRELIMINARY; PRT; 114 AA.
AC Q9UL80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Nerwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035034; AAD56270.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 114
FT NON_TER 114
SQ SEQUENCE 114 AA; 12775 MW; 070E31E21D1CB01 CRC64;

Query Match 29.1%; Score 362; DB 4; Length 114;
Best Local Similarity 60.5%; Pred. No. 3.5e-26;
Matches 69; Conservative 21; Mismatches 22; Indels 2; Gaps 2;

QY 21 DIVLTQSPGTLSPGERATLSCAKSQSDYDGDSTVMNYYQKPGQAPRLIIYAASNL 79
DB 1 DVYMTQSPSLPVTLRQAPASISCRSQSPVSDGTYLNNWFQRPQSPRLIYKVSNRD 60

QY 80 SGIPDRFSGSGGTDFLTISRLEPADFAVYVYCOQSNE-DPRTFGQGRLEIKR 132
DB 61 SGVDRFSGSGGTDFLTISRVEADVGYYVYCOQTHWPPWTFGQGRLEIKR 114

RESULT 14
Q9U410 PRELIMINARY; PRT; 106 AA.
AC Q9U410;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE MONOCLONAL ANTI-IDIOYTPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
OC Schistosoma.
OX NCBI_TaxID=6182;
RN 1
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the light chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF207620; AAF19434.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 1

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Job time: 288 sec

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FT NON_TER 106 106
SQ SEQUENCE 106 AA; 11478 MW; F20F544426BAB63E CRC64;

Query Match      27.8%; Score 345.5; DB 5; Length 106;
Best Local Similarity 61.5%; Pred. No. 1.1e-24;
Matches 67; Conservative 13; Mismatches 24; Indels 5; Gaps 1;

Qy 23 VLTQSPGTLSPGGERATLSCASQSYDYGDSYMNWYQKPGQAPRLIYAASNLESGI 82
Db 3 LTQSPALMSASPGKVTMTCSASSV-----SYVWYTLQKPGSSPRLIYDTSNLASGV 57
Qy 83 PDRESGSGGTDFTLTISRLEPADFAVYYCQSNEDPRFTGGQTRLEIK 131
Db 58 PVRFSGSGGTSYSLTISRMEADAATYYCQWTSYPFTFGSGTKLEK 106

RESULT 15
Q9QYF0 PRELIMINARY; PRT; 298 AA.
AC Q9QYF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CN 8 SCFV.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-SPLEEN;
RA Shinohara N., Demura T., Fukuda H.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-SPLEEN;
RA Shinohara N., Demura T., Fukuda H.;
RT "Isolation of a novel type of vascular cell wall-specific monoclonal
RT antibody recognizing a cell polarity using a phage display subtraction
RT method."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AB036341; BAA8633.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match      26.7%; Score 331; DB 11; Length 298;
Best Local Similarity 46.1%; Pred. No. 8.9e-23;
Matches 70; Conservative 20; Mismatches 40; Indels 22; Gaps 3;

Qy 17 GSTGDIVLTSQSGTSLSPGERATLSCASQSYDYGDSYMNWYQKPGQAPRLIYAAS 76
Db 169 GGGSDIELTQSPASLSASVGETVITCRASGNI-----HNYLAWYQKQKSPQLLVYNAK 224
Qy 77 NLESGIPDRFSGSGGTDFTLTISRLEPADFAVYYCQSNEDPRFTGGQTRLEIKRTVAA 136
Db 225 TLADGVPSRFSGSGGTQYSLKINSIQPEDFGSYQCQHFWTTPYTFGGGTKLEIKRAAG 284
Qy 137 PSVFIFFPSDEQLKSGTASVCLLNFPYREA 168
Db 285 APV-----PYDPLE-----PREA 298
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Search completed: April 24, 2002, 15:13:10



GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 15:09:51 ; Search time 85.18 Seconds
(without alignments)
206.967 Million cell updates/sec

Title: US-09-499-662-52
Perfect score: 1246
Sequence: 1 METDTILLWLLLVPGSTG.....EVTHQGLSPVTKSFNRGEC 238

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1101.*
1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT.*
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16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT.*
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21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	1246	100.0	238	19 AAW83032 Anti-Fas humanised
2	1246	100.0	238	21 AAB14773 Humanised anti-Fas
3	1246	100.0	238	21 AAW90923 Humanised anti-Fas
4	1239	99.4	238	19 AAW83035 Anti-Fas humanised
5	1239	99.4	238	21 AAB14778 Humanised anti-Fas
6	1239	99.4	238	21 AAW90928 Humanised HFE7A de
7	1238	99.4	238	19 AAW83033 Anti-Fas humanised
8	1238	99.4	238	21 AAB14774 Humanised anti-Fas
9	1238	99.4	238	21 AAW90924 Humanised anti-Fas
10	1202	96.5	238	19 AAW83031 Anti-Fas humanised
11	1202	96.5	238	21 AAB14772 Humanised anti-Fas

12	1202	96.5	238	21	AAW90922	Humanised anti-Fas
13	1201	96.4	238	19	AAW83034	Anti-Fas humanised
14	1201	96.4	238	21	AAB14777	Humanised anti-Fas
15	1201	96.4	238	21	AAW90927	Humanised HFE7A de
16	1159	93.0	238	21	AAW90931	Humanised anti-Fas
17	1156	92.8	238	21	AAW90932	Humanised anti-Fas
18	1155	92.7	238	21	AAW90930	Humanised anti-Fas
19	1032.5	82.9	235	21	AAW93702	The kappa chain of
20	1032.5	82.9	235	21	AAW93729	The kappa chain of
21	1032	82.8	235	18	AAW13563	Humanised anti-L-s
22	1029	82.6	234	21	AAW92239	Human bone marrow-
23	1028	82.5	240	20	AAW50161	Human reshaped F19
24	1018	81.7	218	20	AAW95658	Mus musculus anti-
25	1018	81.7	218	21	AAW85200	Light chain amino
26	1018	81.7	218	22	AAW76947	Full variable ligh
27	1018	81.7	234	21	AAW93708	The kappa chain of
28	1018	81.7	234	21	AAW93733	The kappa chain of
29	1015.5	81.5	233	21	AAW93704	The kappa chain of
30	1015.5	81.5	233	21	AAW93731	The kappa chain of
31	1011	81.1	218	14	AAW33312	Humanised MaE11 Ve
32	1007	80.8	237	20	AAW73873	Human antife epsil
33	1001	80.3	240	20	AAW73875	Human antife epsil
34	1000	80.3	236	22	AAW71272	Human gene 2-encod
35	997.5	80.1	384	22	AAU14461	Human novel protei
36	997.5	80.1	384	22	AAU14462	Human novel protei
37	997.5	80.1	384	22	AAU14463	Human novel protei
38	997.5	80.1	384	22	AAU14464	Human novel protei
39	995	79.9	218	20	AAW50030	Human E27 anti-IgE
40	995	79.9	218	20	AAW95660	Mus musculus anti-
41	995	79.9	218	20	AAW95662	Mus musculus anti-
42	995	79.9	218	21	AAW07472	Amino acid sequenc
43	995	79.9	218	22	AAW74211	E27 anti-IgE antib
44	992	79.6	218	20	AAW95669	Mus musculus anti-
45	992	79.6	218	20	AAW95664	Mus musculus anti-

ALIGNMENTS

RESULT 1
AAW83032
ID AAW83032 standard; Protein: 238 AA.

XX AC AAW83032;

XX DT 15-MAR-1999 (first entry)

XX DE Anti-Fas humanised antibody HFE7A light chain HM type.

XX KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
KW systemic lupus erythematosus; graft versus host disease;
KW Sjogren syndrome; pernicious anaemia; Addison's disease;
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KW rheumatoid arthritis; autoimmune haemolytic anaemia;
KW myasthenia gravis; multiple sclerosis; Basedow's disease;
KW thrombopenia purpura; insulin-dependent diabetes; allergy;
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy; AIDS;
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KW transplant rejection; therapy.

XX OS Homo sapiens.

XX Key Synthetic.

XX FH Key Location/Qualifiers

XX FT Peptide 1..20

XX FT Protein /label= Sig_peptide

XX FT Protein 21..238

XX FT Region /label= Mat_protein

XX FT Region 21..131

XX FT Region /label= Variable

XX FT Region 132..238

XX FT Region /label= Constant

QY 1 METDTILLWVLLWVPGSTGDIIVLTQSPGTLSPGERATLSCKASQSVVDYDGSYNNWY 60
 Db 1 metdtillwvllwvpgstgdiivltqspgtlspgeratlsckasqsvdydgsymwy 60
 QY 61 QQKPGQAPRLIIYAASNLSESGIPDRFSGSGGTDFTLTTHPVEEDAATYYCOQSNEDPR 120
 Db 61 qqkpgqaprllyaaanlesgipdrfsgsgsgtdftltthpveeedaatyycqgsnedpr 120
 QY 121 TFGGTRLEIKRTVAAPSVFIFFPPSDQLKSGTASVVCLLNNFYPREAKVQWVDNALQS 180
 Db 121 tfggtrleikrtvaapsvfiffppsdqlksgtasvvcllnnfypreakvqwkvdnalqs 180
 QY 181 GNSQESVTEQDSDKSTYLSSTLTLSKADYKHKVYACEVTHOGLSPVTKSFNRGEC 238
 Db 181 gnsqesvteqsdskstyslstltlskadyekhkvacevthglspsvtksfnrgec 238

RESULT 3
 AAW90923 standard; Protein; 238 AA.
 AC AAW90923;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Humanised anti-Fas antibody HFE7A light chain HM type protein.
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX Synthetic.
 XX
 XX EP90663-A2.
 XX
 XX 05-APR-2000.
 XX
 XX 29-SEP-1999; 99EP-0307711.
 XX
 XX 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX
 XX (SANY) SANKYO CO LTD.
 XX
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 PI WPI; 2000-258930/23.
 DR N-PSDB; AAA11563.
 XX
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems -
 XX
 XX Example reference 14; Page 117-118; 263pp; English.
 XX
 CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive

CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A light chain HM type which is used in
 CC the method described in the invention.

XX Sequence 238 AA;
 SQ

Query Match 100.0%; Score 1246; DB 21; Length 238;
 Best Local Similarity 100.0%; Pred. No. 6.2e-67;
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METDTILLWVLLWVPGSTGDIIVLTQSPGTLSPGERATLSCKASQSVVDYDGSYNNWY 60
 Db 1 metdtillwvllwvpgstgdiivltqspgtlspgeratlsckasqsvdydgsymwy 60
 QY 61 QQKPGQAPRLIIYAASNLSESGIPDRFSGSGGTDFTLTTHPVEEDAATYYCOQSNEDPR 120
 Db 61 qqkpgqaprllyaaanlesgipdrfsgsgsgtdftltthpveeedaatyycqgsnedpr 120
 QY 121 TFGGTRLEIKRTVAAPSVFIFFPPSDQLKSGTASVVCLLNNFYPREAKVQWVDNALQS 180
 Db 121 tfggtrleikrtvaapsvfiffppsdqlksgtasvvcllnnfypreakvqwkvdnalqs 180
 QY 181 GNSQESVTEQDSDKSTYLSSTLTLSKADYKHKVYACEVTHOGLSPVTKSFNRGEC 238
 Db 181 gnsqesvteqsdskstyslstltlskadyekhkvacevthglspsvtksfnrgec 238

RESULT 4
 AAW83035
 ID AAW83035 standard; Protein; 238 AA.
 XX
 AC AAW83035;
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE Anti-Fas humanised antibody HFE7A light chain PDHM type.
 XX
 KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy.

XX Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Peptide 1..20
 FT Protein 21..238
 FT Region 21..131

FT Region /label= Variable
 FT 132..238
 FT /label= Constant
 FT 44..58
 FT /label= CDR_L1
 FT /note= "claim 9"
 FT 74..80
 FT /label= CDR_L2
 FT /note= "claim 9"
 FT 113..121
 FT /label= CDR_L3
 FT /note= "claim 9"
 XX AU9859701-A.
 XX 08-OCT-1998.
 XX 30-MAR-1998; 98AU-0059701.
 XX 08-OCT-1997; 97JP-0276064.
 XX 01-APR-1997; 97JP-0082953.
 XX 25-JUN-1997; 97JP-0169088.
 XX (SANY) SANKYO CO LTD.
 XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 XX Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX WPI; 1998-543440/47.
 XX N-PSDB; AAV70078.
 XX New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX Claim 21; Page 220-221; 292pp; English.
 XX This is the amino acid sequence of the PDHM type humanised light
 CC chain of murine anti-human Fas monoclonal antibody HFE7A.
 CC Humanisation of the murine sequence (see AAW83042) entailed making
 CC DIE, P47A, K49R and R107K amino acid substitutions; these
 CC residues are conserved in the human light (kappa) chain. Host
 CC cell Escherichia coli PHSHM2 SANK 70198 harbors plasmid PHSHM2
 CC carrying a fusion of the humanised PDHM type HFE7A light chain and
 CC DNA encoding the region of human immunoglobulin kappa chain, and is
 CC deposited as FERM BP-6272 (claimed). The invention provides
 CC methods for producing humanised antibodies by culturing host
 CC cells. Humanised versions of HFE7A (see AAW83031-37), like native
 CC HFE7A, are capable of inducing apoptosis in abnormal cells
 CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal
 CC cells. The humanised antibodies are used to evaluate, in animal
 CC models, treatments of diseases that involve Fas/Fas ligand
 CC interactions, and also to treat such diseases, including autoimmune
 CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
 CC graft versus host disease, Sjogren syndrome, pernicious anaemia,
 CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
 CC sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
 CC thrombopenia purpura and insulin-dependent diabetes), allergies,
 CC atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
 CC nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
 CC rejection (all claimed).
 XX Sequence 238 AA;
 XX Query Match 99.4%; Score 1239; DB 19; Length 238;
 XX Best Local Similarity 99.2%; Pred. No. 1.6e-66;
 XX Matches 236; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 METDTILLVLLWVPGSTGDIVLTQSPGTLISLSPGERATLSCASQSDVDYDGDSDYNNWY 60
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1 metdtillvllwvpgstgeivltqspgtlslspgeratlscasqsvdydgdsgymwy 60
 QY 61 QOKPGQAPRLIIYAASNLESIGIPDREGSGSGTDFLTTHPVEEDAATVYCOQSNEDPR 120
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 qkpgqaprllyaaanlesgipdrifsgsgsgtdfclthpveedaatyycqsgnedpr 120
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 121 TFGQTRLEIKRTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPREAKVQWVDNALQS 180
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 tfgggtkkleikrtvaapsvfifppsdeqlksgtasvvcillnnfypreakvqwkvdnalqs 180
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 QY 181 GNSQSVTEQDSKDYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTYKSNRGE 238
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 gnsqesvteqdkdstyslsstltlskadylekhkvacevthqglsspvtksfnrgce 238
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 RESULT 5
 AAB14778
 ID AAB14778 standard; Protein; 238 AA.
 XX AC AAB14778;
 XX AC AAB14778;
 XX 24-NOV-2000 (first entry)
 XX Humanised anti-Fas antibody light chain, SEQ ID NO:109.
 XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; humanised antibody; complementarity determining region; CDR;
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
 KW hepatitis; AIDS; graft rejection; light chain.
 XX Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX JP2000169393-A.
 XX 20-JUN-2000.
 XX 30-SEP-1999; 99JP-0278301.
 XX 30-SEP-1998; 98JP-0276883.
 XX (SANY) SANKYO CO LTD.
 XX WPI: 2000-485645/43.
 XX N-PSDB; AAA72177.
 XX Preventive or treating agent for the diseases caused by an abnormality
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody
 XX Claim 20; Page 103; 139pp; Japanese.
 XX The invention relates to compositions for the prevention or treatment
 CC of diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The compositions of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
 CC represent the light chains of several humanised HFE7A-derived anti-Fas
 CC antibodies.
 XX Sequence 238 AA;
 XX Query Match 99.4%; Score 1239; DB 21; Length 238;

Best Local Similarity 99.2%; Pred. No. 1.6e-66;
Matches 236; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 METDTILLWVLLWVPGSTGDIVLTQSPGTLISLSPGERATISCKASQSDVDGDSYMMWY 60
Db 1 metdtillwvllwvpgstgeivltqspgtlislspgeratiscasqsdvdygdsymw 60

Qy 61 QOKGQAPRLIYAASNLESGIPDRFSGSGSGTDTLTTHPVEEDAATYYCOQSNEDPR 120
Db 61 qqkqgqaprllyaaanlesgipdrfsgsgsgtftltihpveedaatyccqgsnepr 120

Qy 121 TFGGOTRLEIKRTVAAPSFIFFPPSDEQLKSGTASVCLLNFFPREAKVQKVDNALQS 180
Db 121 tfgggtkleikrtvaapsfifppdsedqlksgtasvcllnffpreakvqkvdnalqs 180

Qy 181 GNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 gnsqesvteqdsksdystlsstltlskadyekhkvyacevthqglsspvtksfnrgc 238

RESULT 6
AAW90928
ID AAW90928 standard; Protein: 238 AA.
XX
AC AAW90928;
XX
DT 08-AUG-2000 (first entry)
XX
DE Humanised HFE7A designed light chain protein #2.
XX
Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjogren's syndrome; anaemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX
OS Synthetic.
XX
PN EP990663-A2.
XX
PD 05-APR-2000.
XX
PF 29-SEP-1999; 99EP-0307711.
XX
PR 30-SEP-1998; 98JP-0276881.
PR 30-SEP-1998; 98JP-0276882.
XX
PA (SANY) SANKYO CO LTD.
XX
PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX
WPI: 2000-258930/23.
DR N-PSDB; AAA11615.
DR
XX
FT New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems
XX
PS Example reference 21; Page 144-145; 263pp; English.
XX
CC This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, immunosuppressive, thyromimetic,
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,

CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
CC antiarteriosclerotic, cardiac and hepatropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjogren's syndrome, Goodpasture syndrome, Crohn's
CC anaemia, Addison's disease, scleroderma, pernicious or hypoplastic
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a humanised anti-Fas antibody HFE7A designed light chain which is used in
CC the method described in the invention.

XX SQ Sequence 238 AA;

Query Match 99.4%; Score 1239; DB 21; Length 238;
Best Local Similarity 99.2%; Pred. No. 1.6e-66;
Matches 236; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 METDTILLWVLLWVPGSTGDIVLTQSPGTLISLSPGERATISCKASQSDVDGDSYMMWY 60
Db 1 metdtillwvllwvpgstgeivltqspgtlislspgeratiscasqsdvdygdsymw 60

Qy 61 QOKGQAPRLIYAASNLESGIPDRFSGSGSGTDTLTTHPVEEDAATYYCOQSNEDPR 120
Db 61 qqkqgqaprllyaaanlesgipdrfsgsgsgtftltihpveedaatyccqgsnepr 120

Qy 121 TFGGOTRLEIKRTVAAPSFIFFPPSDEQLKSGTASVCLLNFFPREAKVQKVDNALQS 180
Db 121 tfgggtkleikrtvaapsfifppdsedqlksgtasvcllnffpreakvqkvdnalqs 180

Qy 181 GNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 gnsqesvteqdsksdystlsstltlskadyekhkvyacevthqglsspvtksfnrgc 238

RESULT 7

AAW83033
ID AAW83033 standard; Protein: 238 AA.

XX
AC AAW83033;

XX
DT 15-MAR-1999 (first entry)

XX
DE Anti-Fas humanised antibody HFE7A light chain MM type.

XX
Fas; antibody; mouse; Fas; humanised antibody;
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
KW systemic lupus erythematosus; graft versus host disease;
KW Sjogren syndrome; pernicious anaemia; Addison's disease;
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KW rheumatoid arthritis; autoimmune haemolytic anaemia;
KW myasthenia gravis; multiple sclerosis; Basedow's disease;
KW thrombopenia purpura; insulin-dependent diabetes; allergy;
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KW transplant rejection; therapy.

XX Homo sapiens.

OS Synthetic.

XX
FH Key Location/Qualifiers

FT Peptide 1..20

FT /label= Sig_peptide

FT Protein 21...238
 FT /label= Mat_protein
 FT Region 21...131
 FT /label= Variable
 FT Region 132...238
 FT /label= Constant
 FT Region 44...58
 FT /label= CDR_L1
 FT /note= "claim 9"
 FT 74...80
 FT /label= CDR_L2
 FT /note= "claim 9"
 FT 113...121
 FT /label= CDR_L3
 FT /note= "claim 9"
 XX
 PN AU9859701-A.
 XX
 XX 08-OCT-1998.
 XX
 XX 30-MAR-1998; 98AU-0059701.
 XX
 PR 08-OCT-1997; 97JP-0276064.
 PR 01-APR-1997; 97JP-0082953.
 PR 25-JUN-1997; 97JP-0169088.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX
 DR WPI; 1998-543440/47.
 DR N-PSDB; AAV70076.
 XX
 XX New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX
 PS Claim 21; Page 202; 292pp; English.
 XX
 CC This is the amino acid sequence of the MM type humanised light
 CC chain of murine anti-human Fas monoclonal antibody HFE7A. E. coli
 CC SANK 73697 harbors plasmid PHSCMM6 carrying a fusion fragment of the
 CC humanised MM type HFE7A light chain and DNA encoding the region of
 CC human kappa chain, and is deposited as FERM BP-6071 (claimed). The
 CC invention provides methods for producing humanised antibodies by
 CC culturing host cells. Humanised versions of HFE7A (see AAM83031-37),
 CC like native HFE7A, are capable of inducing apoptosis in abnormal
 CC cells expressing Fas, and of inhibiting Fas-induced apoptosis in
 CC normal cells. The humanised antibodies are used to evaluate, in
 CC animal models, treatments of diseases that involve Fas/Fas ligand
 CC interactions, and also to treat such diseases, including autoimmune
 CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
 CC graft versus host disease, Sjogren syndrome, pernicious anaemia,
 CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
 CC sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
 CC thrombopenia purpura and insulin-dependent diabetes), allergies,
 CC atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
 CC nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
 CC rejection (all claimed).
 XX
 SQ Sequence 238 AA;

Query Match 99.4%; Score 1238; DB 19; Length 238;
 Best Local Similarity 99.2%; Pred. No. 1.8e-66;
 Matches 236; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 METDTILLWLLVVPSTGDIIVLTQSPGTLISLSPGERATLSCRASQSDVDGDSYMMWY 60
 Db 1 metdtillwllvvpstgdivltqspgtlspsgeratlsckasgsvdydgdsmymwy 60

Qy 61 QOKPGQAPRLTIYAASNLSESGIPDRFSGSGGTDTLTTHPVEEDAATYYCQSQNEDPR 120
 Db 61 qkpgqppklliyaasnlesgipdrfsgsgsgtdftltihpveedaatyyccqsgnedpr 120
 Qy 121 TFGQCTRIEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVQNALQS 180
 Db 121 tfggqtrleikrtvaapsvfifppsdeqlksgtasvcllnnfybreakvqwkvdnals 180
 Qy 181 GNSQESVTEODSKDSTYSLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 238
 Db 181 gnsqesvteqsdksdtyglsstltlskadyekhkyacevthqgisspvtksfnrgec 238

RESULT 8

AAB14774
 ID AAB14774 standard; Protein; 238 AA.

XX AC AAB14774;

XX DT 24-NOV-2000 (first entry)

XX DE Humanised anti-Fas antibody light chain, SEQ ID NO:54.

XX KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; humanised antibody; complementarity determining region; CDR;
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
 KW hepatitis; AIDS; graft rejection; light chain.

OS Chimeric - Mus musculus.

OS Chimeric - Homo sapiens.

XX PN JP2000169393-A.

XX PD 20-JUN-2000.

XX PF 30-SEP-1999; 99JP-0278301.

XX FR 30-SEP-1998; 98JP-0276883.

XX PA (SANY) SANKYO CO LTD.

XX WPI; 2000-485645/43.

XX DR N-PSDB; AAA72126.

XX PT Preventive or treating agent for the diseases caused by an abnormality
 in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 anti-Fas antibody

XX PS Claim 20; Page 83; 139pp; Japanese.

XX CC The invention relates to compositions for the prevention or treatment
 or diseases caused by an abnormality in the Fas/Fas ligand system
 containing an anti-Fas antibody as the active component. The anti-Fas
 antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 or a humanised version of HFE7A containing identical CDRs
 (complementarity determining regions) to antibody HFE7A. Via its
 interaction with Fas, the antibody of the invention acts as a modulator
 of apoptosis. The compositions of the invention may therefore be used in
 the treatment or prevention of conditions such as autoimmune diseases,
 allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
 represent the light chains of several humanised HFE7A-derived anti-Fas
 antibodies.

XX SQ Sequence 238 AA;

Query Match 99.4%; Score 1238; DB 21; Length 238;
 Best Local Similarity 99.2%; Pred. No. 1.8e-66;

FT Region /label= Mat_protein
 FT 21..131
 FT /label= Variable
 FT 132..238
 FT /label= Constant
 FT 44..58
 FT /label= CDR_L1
 FT /note= "claim 9"
 FT 74..80
 FT /label= CDR_L2
 FT /note= "claim 9"
 FT 113..121
 FT /label= CDR_L3
 FT /note= "claim 9"
 XX AU9859701-A.
 XX
 PD 08-OCT-1998.
 XX
 XX 30-MAR-1998; 98AU-0059701.
 XX
 XX 08-OCT-1997; 97JP-0276064.
 PR 01-APR-1997; 97JP-0082953.
 XX 25-JUN-1997; 97JP-0169088.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX
 DR WPI; 1998-543440/47.
 DR N-PSDB; AAV70074.
 XX
 XX New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX
 PS Claim 21; Page 199-199; 292pp; English.
 XX
 XX This is the amino acid sequence of the HH type humanised light
 CC chain of murine anti-human Fas monoclonal antibody HFE7A.
 CC Humanisation of the murine sequence (see AAW83042); entailed making
 CC P47A, K49R, H80S, P81R, V82L, E84P, E85A, A87F and T89V amino acid
 CC substitutions; these residues are conserved in the human light
 CC chain (kappa chain). Host cell Escherichia coli PHSGH7 SANK 73497
 CC harbors plasmid PHSGH7 carrying a fusion fragment of the humanised
 CC HH type HFE7A light chain and DNA encoding the region of human
 CC immunoglobulin kappa chain, and is deposited as FERM BP-6073
 CC (claimed). The invention provides methods for producing humanised
 CC antibodies by culturing host cells. Humanised versions of HFE7A
 CC (see AAW83031-37), like native HFE7A, are capable of inducing
 CC apoptosis in abnormal cells expressing Fas, and of inhibiting
 CC Fas-induced apoptosis in normal cells. The humanised antibodies
 CC are used to evaluate, in animal models, treatments of diseases that
 CC involve Fas/Fas ligand interactions, and also to treat such
 CC diseases, including autoimmune disease (e.g. systemic lupus
 CC erythematosus, Hashimoto's disease, graft versus host disease,
 CC Sjogren syndrome, pernicious anaemia, Addison's disease,
 CC scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid
 CC arthritis, autoimmune haemolytic anaemia, sterility, myasthenia
 CC gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura
 CC and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
 XX
 SQ Sequence 238 AA;

Query Match 96.5%; Score 1202; DB 19; Length 238;
 Best Local Similarity 97.1%; Pred. No. 2.5e-64;
 Matches 231; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 METDTILLWVLLWVPGSTGDIVLTQSPGTLSPGERATLSKASQSDVDGDSYMNWY 60
 DQ 1 metdtillwvllwvpgsgtdivltqspgtlslsgperatlsckasqsdvdydgsymwy 60
 QY 61 QOKFGQAPRLIIYAASNLGSGIPDRFSGSGSGTDFTLTIHPVEEDATATYCCQSQNEQPR 120
 DQ 61 qkpgqaprllyaaasnlsgipdrfsgsgsgtdftltisrlpadfavyvccqsgnedpr 120
 QY 121 TFGGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
 DQ 121 tfggtrleikrtvaapsvfifppsqdeqlksgtasvvcclnnfypreakvqwkvdnalq 180
 QY 181 GNSQSVTEQDQKDSYSLSTLTLKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238
 DQ 181 gnsqsvteqdkdstyyslssltslkadyekhkvyacevthqglsspytksfnrgec 238
 RESULT 11
 AAB14772
 ID AAB14772 standard; Protein; 238 AA.
 AC AAB14772;
 XX
 DT 24-NOV-2000 (first entry)
 XX
 DE Humanised anti-Fas antibody light chain, SEQ ID NO:50.
 XX
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; humanised antibody; complementarity determining region; CDR;
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
 KW hepatitis; AIDS; graft rejection; light chain.
 XX
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX
 PN JP2000169393-A.
 XX
 PD 20-JUN-2000.
 XX
 PF 30-SEP-1999; 99JP-0278301.
 XX
 PR 30-SEP-1998; 98JP-0276883.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 DR WPI; 2000-485645/43.
 DR N-PSDB; AAA72124.
 XX
 PT Preventive or treating agent for the diseases caused by an abnormality
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody -
 PS
 PS Claim 20; Page 78-79; 139pp; Japanese.
 CC The invention relates to compositions for the prevention or treatment
 CC of diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The composition of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
 CC represent the light chains of several humanised HFE7A-derived anti-Fas
 CC antibodies.
 XX
 SQ Sequence 238 AA;

FT Peptide 1..20
 FT /label= Sig_peptide
 FT Protein 21..238
 FT /label= Mat_protein
 FT Region 21..131
 FT /label= Variable
 FT Region 132..238
 FT /label= Constant
 FT Region 44..58
 FT /label= CDR_L1
 FT /note= "claim 9"
 FT Region 74..80
 FT /label= CDR_L2
 FT /note= "claim 9"
 FT Region 113..121
 FT /label= CDR_L3
 FT /note= "claim 9"
 XX AU9859701-A.
 XX
 XX 08-OCT-1998.
 XX
 XX 30-MAR-1998; 98AU-0059701.
 XX
 XX 08-OCT-1997; 97JP-0276064.
 XX 01-APR-1997; 97JP-0082953.
 XX 25-JUN-1997; 97JP-0169088.
 XX
 XX (SANY) SANKYO CO LTD.
 XX
 XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 FI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX
 XX WPI: 1998-543440/47.
 XX N-PSDB; AAV70077.
 DR
 DR
 XX
 FT New antibodies and proteins bind conserved epitope of Fas antigen -
 used to evaluate drugs in animal models and to treat Fas-associated
 diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 myocarditis, hepatitis and AIDS
 FT
 FT
 FT
 FT
 FT
 PS Claim 21: Page 218; 292pp; English.
 XX
 XX This is the amino acid sequence of the PDHH type humanised light
 chain of murine anti-human Fas monoclonal antibody HFE7A.
 CC Humanisation of the murine sequence (see AAW83042) entailed making
 CC DIE, P47A, K49R, H80S, P81R, V82L, E84P, A87F, T89V and R107K
 CC amino acid substitutions; these residues are conserved in the
 CC human light chain (kappa chain). Host cell Escherichia coli
 CC pSHH5 SANK 70398 harbors plasmid pSHH5 carrying a fusion
 CC fragment of the humanised PDHH type HFE7A light chain and DNA
 CC encoding the region of human immunoglobulin kappa chain, and is
 CC deposited as FERM Bp-6274 (claimed). The invention provides
 CC methods for producing humanised antibodies by culturing host
 CC cells. Humanised versions of HFE7A (see AAW83031-37), like native
 CC HFE7A, are capable of inducing apoptosis in abnormal cells
 CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal
 CC cells. The humanised antibodies are used to evaluate, in animal
 CC models, treatments of diseases that involve Fas/Fas ligand
 CC interactions, and also to treat such diseases, including autoimmune
 CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
 CC graft versus host disease, Sjogren syndrome, pernicious anaemia,
 CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
 CC sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
 CC thrombopenia purpura and insulin-dependent diabetes), allergies,
 CC atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
 CC nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
 CC rejection (all claimed).
 XX
 XX Sequence 238 AA;

Query Match 96.4%; Score 1201; DB 19; Length 238;
 Best Local Similarity 96.6%; Pred. No. 2.8e-64;
 Matches 230; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 METDTILLWVLLVWPGSTGDIVLTQSPGTLSLSPGERATLSCAKASQSVVDYDGDSYMNY 60
 Db 1 metdtillwvllwvpgstgeivltqspgtlsispggeratlsckasqsvdydgdSYMNY 60
 Qy 61 OOKPGQAPRLITYAASNEESGIPDRFSGSGGTDFTLTHHPVEEEDAAITYYCQSQSNEPR 120
 Db 61 qkpqgqaprlityaasnjesgipdrfsgsggtdfTLTLTLTLTLTLTLTLTLTLTLTLTL 120
 Qy 121 TFGQTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQ 180
 Db 121 tfggtrleikrtvaapsyfifppsdqksgtasvcllnnfyprEAKVQWKVDNALQ 180
 Qy 181 GNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 238
 Db 181 gnsqesvteqgskdstylstltlskadyekhkvyacevthqglsspvtksfnrgeC 238
 RESULT 14
 AAB14777
 ID AAB14777 standard; Protein; 238 AA.
 XX
 AC AAB14777;
 XX
 DT 24-NOV-2000 (first entry)
 XX
 DE Humanised anti-Fas antibody light chain, SEQ ID NO:107.
 XX
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; humanised antibody; complementarity determining region; CDR;
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
 KW hepatitis; AIDS; graft rejection; light chain.
 XX
 OS Chimeric - Mus musculus
 OS Chimeric - Homo sapiens
 XX
 PN JP2000169393-A.
 XX
 XX 20-JUN-2000.
 XX
 PF 30-SEP-1999; 99JP-0278301.
 XX
 PR 30-SEP-1998; 98JP-0276883.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 DR WPI: 2000-485645/43.
 DR N-PSDB; AAA72176.
 XX
 PT Preventive or treating agent for the diseases caused by an abnormality
 in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 anti-Fas antibody
 XX
 PS Claim 20; Page 101; 139pp; Japanese.
 XX
 CC The invention relates to compositions for the prevention or treatment
 or diseases caused by an abnormality in the Fas/Fas ligand system
 containing an anti-Fas antibody as the active component. The anti-Fas
 antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 or a humanised version of HFE7A containing identical CDRs
 (complementarity determining regions) to antibody HFE7A. Via its
 interaction with Fas, the antibody of the invention acts as a modulator
 of apoptosis. The compositions of the invention may therefore be used in
 the treatment or prevention of conditions such as autoimmune diseases,
 allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 and organ graft rejection. Sequences AAB14777-B14778 and AAB14777-B14778
 represent the light chains of several humanised HFE7A-derived anti-Fas

CC antibodies.
 XX Sequence 238 AA;
 SQ

Query Match 96.4%; Score 1201; DB 21; Length 238;
 Best Local Similarity 96.6%; Pred. No. 2.8e-64;
 Matches 230; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 METDTILLWLLWVPGSTGDIVLTQSPGTLISLSPGERATLSCSKASQSDVDGDSYNNWY 60
 DB 1 metdtillwllwvpstgeivltqspgtlslspgeratlscskasqsdvdgdsymnw 60

QY 61 QOKPGQAPRLIIYAASNLESGIPDRFSGSGGTDTLTTHPVEEEDAATYCCQOSNEDPR 120
 DB 61 qkpgqaprllyaaanlesgipdrfsgsgsgtdftltisrlepedfavyycqgsnedpr 120

QY 121 TFGGOTRLEIKRTVAAPSVFIFFPSDQLKSGTASVVCLLNNFYPRAKQVQKVDNALQS 180
 DB 121 tfgggtkleikrtvaapsvfifpssdeqlksgtasvvccllnnfyprkakvqkvdnalqs 180

QY 181 GNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 DB 181 gnsqesvteqdsksdystlslstltlskadyekhkvyacevthqglsspvtksfnrgec 238

RESULT 15
 AAW90927
 ID AAW90927 standard; Protein; 238 AA.
 XX
 AC AAW90927;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Humanised HFE7A designed light chain protein.
 XX
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX
 OS Synthetic.
 XX
 XX EP990663-A2.
 XX
 XX 05-APR-2000.
 XX
 XX 29-SEP-1999; 99EP-0307711.
 XX
 XX 30-SEP-1998; 98JP-0276881.
 XX
 XX 30-SEP-1998; 98JP-0276882.
 XX
 XX (SANY) SANKYO CO LTD.
 XX
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX
 XX WPI: 2000-258930/23.
 XX
 XX N-PSDB: AAA11614.
 XX
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 XX inflammatory or autoimmune disease, induces apoptosis selectively in
 XX cells with abnormal Fas-Fas ligand systems
 XX
 XX Claim 3; Page 141-142; 263pp; English.
 XX
 XX This invention describes a novel humanized anti-Fas antibody-like

molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antiinfertility, neuroprotective, antiarteriosclerotic, cardiant and hepatotropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody HFE7A designed light chain which is used in the method described in the invention.

CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatotropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A designed light chain which is used in
 CC the method described in the invention.
 XX
 SQ Sequence 238 AA;

Search completed: April 24, 2002, 15:09:52
 Job time: 95 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 15:10:40 ; Search time 42.08 seconds
(without alignments)
127.276 Million cell updates/sec

Title: US-09-499-662-52
Perfect score: 1246
Sequence: 1 METDRIILLWLLVPGSTG.....EVTHGLSPVTKSFNRGEC 238

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1032	82.8	218	5	PCT-US96-13152-2
2	1018	81.7	218	3	US-08-887-352B-13
3	1018	81.7	218	3	US-08-466-151-9
4	1018	81.7	218	4	US-09-109-207C-13
5	1018	81.7	218	4	US-09-296-005-13
6	995	79.9	218	4	US-09-282-505-1
7	995	79.9	218	4	US-09-054-255-1
8	992	79.6	218	2	US-08-887-352B-15
9	992	79.6	218	2	US-08-887-352B-17
10	992	79.6	218	2	US-08-887-352B-19
11	992	79.6	218	2	US-08-887-352B-24
12	992	79.6	218	4	US-09-109-207C-15
13	992	79.6	218	4	US-09-109-207C-17
14	992	79.6	218	4	US-09-109-207C-19
15	992	79.6	218	4	US-09-109-207C-24
16	992	79.6	218	4	US-09-296-005-15
17	992	79.6	218	4	US-09-296-005-17
18	992	79.6	218	4	US-09-296-005-19
19	992	79.6	218	4	US-09-296-005-24
20	969.5	77.8	241	2	US-07-916-098A-56
21	965.5	77.5	239	3	US-08-487-550-6
22	959	77.0	234	4	US-09-049-672A-6
23	940.5	75.5	233	2	US-07-934-373C-25
24	940.5	75.5	233	3	US-08-437-642B-25
25	940.5	75.5	233	5	PCT-US93-07832-25
26	940.5	75.5	235	4	US-09-171-945-97
27	937	75.2	214	2	US-07-934-373C-39

28	937	75.2	214	3	US-08-437-642B-39	Sequence 39, Appl
29	937	75.2	214	5	PCT-US93-07832-39	Sequence 39, Appl
30	935.5	75.1	235	1	US-08-276-852-153	Sequence 153, App
31	935.5	75.1	235	1	US-08-899-575-153	Sequence 153, App
32	935.5	75.1	235	1	US-08-899-575-153	Sequence 153, App
33	935.5	75.1	235	5	PCT-US95-08743-153	Sequence 153, App
34	932.5	74.8	235	4	US-09-171-945-99	Sequence 99, Appl
35	932	74.8	214	2	US-07-934-373C-40	Sequence 40, Appl
36	932	74.8	214	2	US-08-788-800-11	Sequence 11, Appl
37	932	74.8	214	3	US-08-437-642B-40	Sequence 40, Appl
38	932	74.8	214	3	US-09-097-309-2	Sequence 2, Appl
39	932	74.8	214	4	US-09-097-171A-2	Sequence 2, Appl
40	932	74.8	214	5	PCT-US93-07832-40	Sequence 40, Appl
41	932	74.8	237	3	US-09-097-309-6	Sequence 6, Appl
42	932	74.8	237	4	US-09-097-171A-10	Sequence 10, Appl
43	932	74.8	237	4	US-09-422-712B-2	Sequence 2, Appl
44	932	74.8	237	4	US-09-607-756-2	Sequence 2, Appl
45	931.5	74.8	235	4	US-09-171-945-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
PCT-US96-13152-2
; Sequence 2, Application PE/TUS9613152
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich, et al.
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; ADDRESSEE: Attn: Norman D. Hanson
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13152
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: 27-Dec-95
; APPLICATION NUMBER: EP 95 112 895.8
; FILING DATE: 17-Aug-95
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 19-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Norman D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-13152-2

Query Match 82.8%; Score 1032; DB 5; Length 218;
Best Local Similarity 89.9%; Pred. No. 8.7e-79;

QY 141 IFPPSDEQLKSGTASVCLLNPFYPRKAVQWVDNALQSGNSQESVTEQDSKDSYLS 200
Db 121 IFPPSDEQLKSGTASVCLLNPFYPRKAVQWVDNALQSGNSQESVTEQDSKDSYLS 180
QY 201 STLTSLKADYEKKHVYACEVTHOGLSSPVTKSFNRGEC 238
Db 181 STLTSLKADYEKKHVYACEVTHOGLSSPVTKSFNRGEC 218

RESULT 4
US-09-109-207C-13
; Sequence 13, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-13

Query Match 81.7%; Score 1018; DB 4; Length 218;
Best Local Similarity 88.5%; Pred. No. 1.3e-77;
Matches 193; Conservative 13; Mismatches 12; Indels 0; Gaps 0;
QY 21 DIVLTQSPGTLSPGERATLSCASQSDYDGDSDYNNWYQKPGQAPRLIIYAASNLES 80
Db 1 DIQLTQSPSSLASVSGDRVTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIIYAASYLE 60
QY 81 GIPDRFSGSGSGTDFTLTITHPVEEEDAAATYYCOQSNEDPRTFGQGTREIKRTVAAPSVF 140
Db 61 GVPDRFSGSGSGTDFTLTITSSLPQEDFATYYCOQSHEDPVTFGQGTREIKRTVAAPSVF 120
QY 141 IFPPSDEQLKSGTASVCLLNPFYPRKAVQWVDNALQSGNSQESVTEQDSKDSYLS 200
Db 121 IFPPSDEQLKSGTASVCLLNPFYPRKAVQWVDNALQSGNSQESVTEQDSKDSYLS 180
QY 201 STLTSLKADYEKKHVYACEVTHOGLSSPVTKSFNRGEC 238
Db 181 STLTSLKADYEKKHVYACEVTHOGLSSPVTKSFNRGEC 218

RESULT 5
US-09-296-005-13
; Sequence 13, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial

; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-296-005-13

Query Match 81.7%; Score 1018; DB 4; Length 218;
Best Local Similarity 88.5%; Pred. No. 1.3e-77;
Matches 193; Conservative 13; Mismatches 12; Indels 0; Gaps 0;
QY 21 DIVLTQSPGTLSPGERATLSCASQSDYDGDSDYNNWYQKPGQAPRLIIYAASNLES 80
Db 1 DIQLTQSPSSLASVSGDRVTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIIYAASYLE 60
QY 81 GIPDRFSGSGSGTDFTLTITHPVEEEDAAATYYCOQSNEDPRTFGQGTREIKRTVAAPSVF 140
Db 61 GVPDRFSGSGSGTDFTLTITSSLPQEDFATYYCOQSHEDPVTFGQGTREIKRTVAAPSVF 120
QY 141 IFPPSDEQLKSGTASVCLLNPFYPRKAVQWVDNALQSGNSQESVTEQDSKDSYLS 200
Db 121 IFPPSDEQLKSGTASVCLLNPFYPRKAVQWVDNALQSGNSQESVTEQDSKDSYLS 180
QY 201 STLTSLKADYEKKHVYACEVTHOGLSSPVTKSFNRGEC 238
Db 181 STLTSLKADYEKKHVYACEVTHOGLSSPVTKSFNRGEC 218

RESULT 6
US-09-282-505-1
; Sequence 1, Application US/09282505A
; Patent No. 6194551
; GENERAL INFORMATION:
; APPLICANT: Eschoe Ekinaduese Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R1
; CURRENT APPLICATION NUMBER: US/09/282,505A
; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-218
; OTHER INFORMATION: Sequence is completely synthesized
US-09-282-505-1

Query Match 79.9%; Score 995; DB 4; Length 218;
Best Local Similarity 86.7%; Pred. No. 1e-75;
Matches 189; Conservative 15; Mismatches 14; Indels 0; Gaps 0;
QY 21 DIVLTQSPGTLSPGERATLSCASQSDYDGDSDYNNWYQKPGQAPRLIIYAASNLES 80
Db 1 DIQLTQSPSSLASVSGDRVTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIIYAASYLE 60
QY 81 GIPDRFSGSGSGTDFTLTITHPVEEEDAAATYYCOQSNEDPRTFGQGTREIKRTVAAPSVF 140
Db 61 GVPDRFSGSGSGTDFTLTITSSLPQEDFATYYCOQSHEDPVTFGQGTREIKRTVAAPSVF 120
QY 141 IFPPSDEQLKSGTASVCLLNPFYPRKAVQWVDNALQSGNSQESVTEQDSKDSYLS 200
Db 121 IFPPSDEQLKSGTASVCLLNPFYPRKAVQWVDNALQSGNSQESVTEQDSKDSYLS 180
QY 201 STLTSLKADYEKKHVYACEVTHOGLSSPVTKSFNRGEC 238
Db 181 STLTSLKADYEKKHVYACEVTHOGLSSPVTKSFNRGEC 218

RESULT 7
US-09-054-255-1
; Sequence 1, Application US/09054255

```

; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-887-352B-15

Query Match 79.6%; Score 992; DB 2; Length 218;
Best Local Similarity 86.2%; Pred. No. 1.8e-75;
Matches 188; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 21 DIVLTQSPGTLSLSPGERATLSCAKSQSYVDYDGDSDYNNWYQOKPGQAPRLIIYAAASNLES 80
  || ||||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 1 DIQLTQSPSLASGVDRVTITCRASKPVDGEGDSYLNWYQOKPGKAPKLLIYAAASYLES 60
  || ||||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
QY 81 GIPDRFSGSGGTDFLTITHPVEEEDAAITYCQSQNSNEDPRTEGQGTRLRLEIKRTVAAPSVF 140
  || ||||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 61 GVPRESFGSGGTDFLTITSSLPQEDFATYYCQSHEDPYTFQGQTKVEIKRTVAAPSVF 120
  || ||||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
QY 141 IPPPDEQLKSGTASVGLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSDSTYSLS 200
  || ||||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 121 IPPPDEQLKSGTASVGLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSDSTYSLS 180
  || ||||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
QY 201 STLTLSKADYERKHVYACEVTHQGLSSPYTKSFNRGEC 238
  || ||||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 181 STLTLSKADYERKHVYACEVTHQGLSSPYTKSFNRGEC 218
  || ||||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

RESULT 9
US-08-887-352B-17
; Sequence 17, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; NUMBER OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-887-352B-17

Query Match 79.6%; Score 992; DB 2; Length 218;
Best Local Similarity 86.2%; Pred. No. 1.8e-75;
Matches 188; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 21 DIVLTQSPGTLSLSPGERATLSCAKSQSYVDYDGDSDYNNWYQOKPGQAPRLIIYAAASNLES 80
  || ||||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 1 DIQLTQSPSLASGVDRVTITCRASKPVDGEGDSYLNWYQOKPGKAPKLLIYAAASYLES 60
  || ||||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
QY 201 STLTLSKADYERKHVYACEVTHQGLSSPYTKSFNRGEC 238
  || ||||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 181 STLTLSKADYERKHVYACEVTHQGLSSPYTKSFNRGEC 218
  || ||||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||


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QY 81 GIPDRFSGSGGDTFTLTTHPVEEEDAATYYCOOSNEDPRTFGQGTREIKRTVAAPSVF 140
Db 61 GVPDRFSGSGGDTFTLTISLQPEDFATYYCOOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
QY 141 IFPPDEQLKSGTASVYVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 200
Db 121 IFPPDEQLKSGTASVYVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
QY 201 STLTLSKADYKHKVACEVTHOGLSSPVTKSFNRGEC 238
Db 181 STLTLSKADYKHKVACEVTHOGLSSPVTKSFNRGEC 218

RESULT 10
US-08-887-352B-19
; Sequence 19, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-19

Query Match 79.6%; Score 992; DB 2; Length 218;
Best Local Similarity 86.2%; Pred. No. 1.8e-75;
Matches 188; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 21 DIVLTQSPGTLSPGERATLSCASQSDYDGDSTNNWYQKPGQAPRLIIYAASNLES 80
Db 1 DIQLTQSPSLASVGDRTVITCRASPKVDGSDYLNWYQKPGKAPKLLIIYAASYLE 60
QY 81 GIPDRFSGSGGDTFTLTTHPVEEEDAATYYCOOSNEDPRTFGQGTREIKRTVAAPSVF 140
Db 61 GVPDRFSGSGGDTFTLTISLQPEDFATYYCOOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
QY 141 IFPPDEQLKSGTASVYVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 200
Db 121 IFPPDEQLKSGTASVYVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
QY 201 STLTLSKADYKHKVACEVTHOGLSSPVTKSFNRGEC 238
Db 181 STLTLSKADYKHKVACEVTHOGLSSPVTKSFNRGEC 218
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RESULT 11
US-08-887-352B-24
; Sequence 24, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-24

Query Match 79.6%; Score 992; DB 2; Length 218;
Best Local Similarity 86.2%; Pred. No. 1.8e-75;
Matches 188; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 21 DIVLTQSPGTLSPGERATLSCASQSDYDGDSTNNWYQKPGQAPRLIIYAASNLES 80
Db 1 DIQLTQSPSLASVGDRTVITCRASPKVDGSDYLNWYQKPGKAPKLLIIYAASYLE 60
QY 81 GIPDRFSGSGGDTFTLTTHPVEEEDAATYYCOOSNEDPRTFGQGTREIKRTVAAPSVF 140
Db 61 GVPDRFSGSGGDTFTLTISLQPEDFATYYCOOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
QY 141 IFPPDEQLKSGTASVYVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 200
Db 121 IFPPDEQLKSGTASVYVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
QY 201 STLTLSKADYKHKVACEVTHOGLSSPVTKSFNRGEC 238
Db 181 STLTLSKADYKHKVACEVTHOGLSSPVTKSFNRGEC 218

RESULT 12
US-09-109-207C-15
; Sequence 15, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypep
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
```


US-09-109-207C-24

Query Match 79.6%; Score 992; DB 4; Length 218;
Best Local Similarity 86.2%; Pred. No. 1.8e-75;
Matches 188; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

Qy	21	DIVLTQSPGTLSSPGERATLSCCKASQSVYDGDSDYNNWYQQKPKGQAPRLIIYAASNLES	80
Db	1	DIQLTQSPFSLASVGDRTITCRASKPVDEGDSYLNWYQQKPKGAPKLLIYAASYLE	60
Qy	81	GIPDRFSGSGGTDFLTITHPVEEEDAATYYCQOSNEDPRTFGQGTREIKRTVAAPSVF	140
Db	61	GVPSRFSGSGGTDFLTITSLQPEDFATYYCQOSHEDPVTFGQGTKEIKRTVAAPSVF	120
Qy	141	IFPPSDQLKSGTASVVCCLNNFYPRKAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS	200
Db	121	IFPPSDQLKSGTASVVCCLNNFYPRKAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLS	180
Qy	201	STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC	238
Db	181	STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC	218

Search completed: April 24, 2002, 15:10:40
Job time: 143 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 15:11:36 ; Search time 49.97 Seconds
(without alignments)
362.809 Million cell updates/sec

Title: US-09-499-662-52

Perfect score: 1246

Sequence: 1 METDTILLWLLWVGSTG.....EVTHOGLSPVTKSPNRGEC 238

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	962.5	77.2	215	2 JE0242	Ig kappa chain NIG
2	927.5	74.4	215	2 JE0244	Ig kappa chain NIG
3	902.5	72.4	215	2 JE0243	Ig kappa chain NIG
4	900.5	72.3	215	2 A23746	Ig kappa chain V-I
5	878	70.5	216	2 JE0241	Ig kappa chain Am3
6	795	63.8	240	2 S06084	Ig kappa chain pre
7	776	62.3	218	2 S68241	Ig kappa chain V r
8	774	62.1	218	2 JC5810	monoclonal antibody
9	759	60.9	210	2 A56169	Ig kappa chain V r
10	717	57.5	220	2 A31790	Ig kappa chain V r
11	713	57.2	234	2 S14237	Ig kappa chain pre
12	712.5	57.2	230	2 S33161	Ig kappa chain - s
13	707.5	56.8	219	2 PC4203	Ig kappa chain (mo
14	704.5	56.5	219	2 S52028	Ig kappa chain - m
15	702.5	56.4	225	2 S37484	Ig kappa chain - m
16	700.5	56.2	219	2 S38865	Ig kappa chain - m
17	699.5	56.1	235	2 S25058	Ig kappa chain - m
18	691.5	55.5	217	2 S42772	Ig kappa chain - m
19	691.5	55.5	219	2 S16112	Ig kappa chain V r
20	687	55.1	214	2 S68212	Ig kappa chain (Wa
21	686	55.1	234	2 S01320	Ig kappa chain pre
22	677.5	54.4	225	2 JL0029	Ig kappa chain pre
23	624	50.1	178	2 PT0219	Ig kappa chain V-C
24	615	49.4	131	2 PH1226	Ig kappa chain pre
25	606.5	48.7	197	2 S29593	Ig kappa chain (WM
26	602.5	48.4	135	2 S52059	JC-kappa protein -
27	591.5	47.5	229	2 A20969	Ig kappa chain pre
28	565.5	45.4	238	2 A49633	Ig lambda-like cha
29	549	44.1	144	2 PL0106	Ig kappa chain pre

```

30      548      44.0      106      1      K3HU      Ig kappa chain C r
31      548      44.0      131      1      KVM5M6      Ig kappa chain pre
32      542      43.5      140      2      PNO446      Ig kappa chain pre
33      533      42.8      131      2      S55027      Ig light chain pre
34      529      42.5      132      1      KVM532      Ig kappa chain pre
35      523.5      42.0      145      2      S20631      Ig kappa chain - h
36      517      41.5      111      1      KVM543      Ig kappa chain V r
37      515      41.3      111      1      KVM583      Ig kappa chain V r
38      513      41.2      99      2      A37927      Ig kappa chain C r
39      513      41.2      111      1      KVM508      Ig kappa chain V r
40      512      41.1      112      2      S19971      Ig kappa chain V r
41      511      41.0      233      2      S29577      Ig light chain - r
42      510      40.9      111      1      KVM569      Ig kappa chain V r
43      507      40.7      99      2      S26653      Ig kappa chain C r
44      502      40.3      111      1      KVM5C1      Ig kappa chain V r
45      500.5      40.2      129      1      K3HUHA      Ig kappa chain pre

```

ALIGNMENTS

RESULT 1

JE0242

Ig kappa chain NIG26 precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JE0242

R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinod

submitted to JIPID, November 1998

A:Description: Structure relationship of kappa type light chains with AL amyloidosis:

A:Reference number: JE0241

A:Accession: JE0242

A:Molecule type: protein

A:Residues: 1-215 <ALI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 77.2%; Score 962.5; DB 2; Length 215;

Best Local Similarity 86.2%; Pred. No. 5.1e-56;

Matches 188; Conservative 11; Mismatches 16; Indels 3; Gaps 1;

```

QY      21      DIVLTQSPGTLISLSPGERATLSCSKASQSDYDGSYMNWYQKPGQAPRLLIYAASNDLES 80
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1      EIVLTQSPGTLISLSPGERATLSCRASQSV---SNNYLAWYQKPGQAPSLLIYDASSRAT 57
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      81      GIPDRFSGSGSDFTLTTHPVEEDATYTCQSNEDPRTFGGQTRLEIKRTVAAPSVF 140
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      58      GIPDRFSGSGSDFTLTISGLEPFAVYCYQYDRPPWTFGGQTKVEIKRTVAAPSVF 117
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      141     IFPPSDQLKSGTASVYVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKOSTYSL 200
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      118     IFPPSDQLKSGTASVYVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKOSTYSL 177
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      201     STLTLSKADYEKKHVKYACEVTHOGLSSPVTKSFNRGEC 238
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      178     STLTLSKADYEKKHVKYACEVTHOGLSSPVTKSFNRGEC 215
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 2

JE0244

Ig kappa chain NIG2 precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JE0244

R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazu, H

submitted to JIPID, November 1998

A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL

A:Reference number: JE0243

A:Accession: JE0244

A:Molecule type: protein

A:Residues: 1-215 <ALI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

[illegible]

QY 21 DIVLTQSPGTLSPGGERATLSCASQSDVDGSDSYMMWYQOKPGQAPRLLIYAASNL 80
Db 1 DIVLTQSPASLTSLGQRATISCRASKSVSSGYSMHWYQOKPGQPKVLIYLAASNL 60
QY 81 GIPDRFSGSGGTDTFTLTHPVEEADAATYCCQSNEDPRTFGGTRELEIKRTVAAPS 140
Db 61 GVPFRFSGSGGTDTFTLTHPVEEADAATYCCQSNEDPRTFGGTRELEIKRTVAAPS 120
QY 141 IFPPSDEOLKSGTASVCLLNFPYPRKAVQKVDNALQSGNSQESVTEQDSKDSYSL 200
Db 121 IFPPSDEOLKSGTASVCLLNFPYPRKAVQKVDNALQSGNSQESVTEQDSKDSYSL 180
QY 201 STLTSLKADYKHKVYACEVTHQGLSPV 229
Db 181 STLTSLKADYKHKVYACEVTHQGLSPV 209

RESULT 10

A31790

Ig kappa chain V region (17/9) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000

C:Accession: A31790

R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.

J. Biol. Chem. 263, 17100-17105, 1988

A:Title: Preliminary crystallographic data, primary sequence, and binding data for an

A:Reference number: A92686; MUID:89034213

A:Accession: A31790

A:Molecule type: mRNA

A:Residues: 1-220 <SCH>

A:Cross-references: GB:M23626; GB:J04061; NID:g533234; PIDN:AAA39162.1; PID:g533235

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 57.5%; Score 717; DB 2; Length 220;

Best Local Similarity 60.5%; Pred. No. 4.8e-40;

Matches 133; Conservative 34; Mismatches 51; Indels 2; Gaps 1;

QY 21 DIVLTQSPGTLSPGGERATLSCASQSDVDG--DSYMMWYQOKPGQAPRLLIYAASNL 78

Db 1 DIVLTQSPSLTVTAGEKVTMSCTSSLSFNKQKYLWYQOKPGQPKVLIYWASTR 60

QY 79 ESGIPDRFSGSGGTDTFTLTHPVEEADAATYCCQSNEDPRTFGGTRELEIKRTVAAPS 138

Db 61 ESGVPRDFTGSGGTDTFTLTHPVEEADAATYCCQSNEDPRTFGGTRELEIKRTVAAPS 120

QY 139 VFIFPPSDEOLKSGTASVCLLNFPYPRKAVQKVDNALQSGNSQESVTEQDSKDSYSL 198

Db 121 VFIFPPSDEOLKSGTASVCLLNFPYPRKAVQKVDNALQSGNSQESVTEQDSKDSYSL 180

QY 199 LSSTLTSLKADYKHKVYACEVTHQGLSPVTKSFNRGEC 238

Db 181 MSSTLTSLKADYKHKVYACEVTHQGLSPVTKSFNRGEC 220

RESULT 11

I4237

Ig kappa chain precursor (15C5) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: I4237

R:Van Damme, A.M.; Buleens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.

Eur. J. Biochem. 192, 767-775, 1990

A:Title: Construction and characterization of a recombinant murine monoclonal antibody

A:Reference number: I4236; MUID:91006173

A:Accession: I4237

A:Molecule type: mRNA

A:Residues: 1-234 <VAN>

A:Cross-references: EMBL:X56394; NID:g51622; PIDN:CAA39805.1; PID:g51623

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 57.2%; Score 713; DB 2; Length 234;

Best Local Similarity 56.3%; Pred. No. 9.3e-40;

Matches 134; Conservative 37; Mismatches 63; Indels 4; Gaps 1;

QY 1 METDTLLWVLLWVPGSTGDIVLTQSPGTLSPGGERATLSCASQSDVDGSDSYMMWY 60

Db 1 MRTAQFLGILLWVPGSTGDIVLTQSPGTLSPGGERATLSCASQSDVDGSDSYMMWY 56

QY 61 QOKPGQAPRLLIYAASNLGSGGTDTFTLTHPVEEADAATYCCQSNEDPRTFGGTRE 120

Db 57 QOKPGKSPKTLIYGRNLRVAGVPSRFSGSGGQDYSLTISSEYEDGVYICLYRDEPFF 116

QY 121 TFGGTRELEIKRTVAAPSVFIFPPSDEOLKSGTASVCLLNFPYPRKAVQKVDNALQ 180

Db 117 TFGGTRELEIKRTVAAPSVFIFPPSDEOLKSGTASVCLLNFPYPRKAVQKVDNALQ 176

QY 181 GNSQESVTEQDSKDSYSLSTLTSLKADYKHKVYACEVTHQGLSPVTKSFNRGEC 238

Db 177 NGVLSNWTQDSKDSYSLSTLTSLKADYKHKVYACEVTHQGLSPVTKSFNRGEC 234

RESULT 12

S33161

Ig kappa chain - sheep

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000

C:Accession: S33161

R:Foley, R.C.; Beh, K.J.

submitted to the EMBL Data Library, July 1990

A:Description: Isolation and characterisation of sheep kappa light chain cDNA.

A:Reference number: S33161

A:Accession: S33161

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-230 <FOL>

A:Cross-references: EMBL:X54110; NID:g297103; PIDN:CAA38046.1; PID:g1364221

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:143-212/Domain: immunoglobulin homology <IMM>

Query Match 57.2%; Score 712.5; DB 2; Length 230;

Best Local Similarity 58.4%; Pred. No. 9.8e-40;

Matches 136; Conservative 38; Mismatches 54; Indels 5; Gaps 2;

QY 7 LLWVLLW-VPGSTGDIVLTQSPGTLSPGGERATLSCASQSDVDGSDSYMMWYQOKPG 65

Db 2 LLGILLWLLPVGARCDIQVTPSPSSLSASLTERVSTCRSSQSV---SNYLNWYQOKPG 57

QY 66 QAPRLLIYAASNLGSGGTDTFTLTHPVEEADAATYCCQSNEDPRTFGGTRE 125

Db 58 QAPKLLIYATRLHTDVPFRFSGSGGTDTFTLTHPVEEADAATYCCQSNEDPRTFGGTRE 117

QY 126 TRLEIKRTVAAPSVFIFPPSDEOLKSGTASVCLLNFPYPRKAVQKVDNALQSGNSQ 185

Db 118 TNVEIKRSDAQPSPVFLFKPSEQLRTGTVSVCLNDFYPRDINVKVDGVTQNSFNQ 177

QY 186 SVTEQDSKDSYSLSTLTSLKADYKHKVYACEVTHQGLSPVTKSFNRGEC 238

Db 178 SFTDQDSKDSYSLSTLTSLKADYKHKVYACEVTHQGLSPVTKSFNRGEC 230

RESULT 13

PC4203

Ig kappa chain (monoclonal antibody MabA34) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000

C:Accession: PC4203

R:Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.

Gene 173, 257-259, 1996

F;1-112/Domain: V region #status predicted <VRG>
F;113-219/Domain: C region #status predicted <CRG>

Db 181 SSTLTLTKEYERHNSYTCEATHKSTSTPIVKSFNREC 219

Search completed: April 24, 2002, 15:11:37
Job time: 195 sec

Result No.	Query No.	%		DB	ID	Description
		Score	Match			
1	548	44.0	106	1	KAC_HUMAN	P01834 homo sapien
2	548	44.0	131	1	KV3I_MOUSE	P01661 mus musculus
3	529	42.5	132	1	KV3F_MOUSE	P01658 mus musculus
4	517	41.5	111	1	KV3M_MOUSE	P01665 mus musculus
5	515	41.3	111	1	KV3N_MOUSE	P01666 mus musculus
6	513	41.2	111	1	KV3O_MOUSE	P01667 mus musculus
7	510	40.9	111	1	KV3Q_MOUSE	P01669 mus musculus
8	502	40.3	111	1	KV3L_MOUSE	P01664 mus musculus
9	500.5	40.2	129	1	KV3L_HUMAN	P01835 homo sapien
10	492.5	39.5	110	1	KV3P_MOUSE	P01668 mus musculus
11	487.5	39.1	129	1	KV3M_HUMAN	P01836 homo sapien
12	454	36.4	111	1	KV3R_MOUSE	P01670 mus musculus
13	453	36.4	128	1	KV3K_HUMAN	P06311 homo sapien
14	450	36.1	111	1	KV3H_MOUSE	P01660 mus musculus
15	446	35.8	111	1	KV3S_MOUSE	P01671 mus musculus
16	443	35.6	111	1	KV3J_MOUSE	P01662 mus musculus
17	442.5	35.5	129	1	KV3H_HUMAN	P04207 homo sapien
18	442	35.5	111	1	KV3K_MOUSE	P01663 mus musculus
19	440	35.3	111	1	KV3T_MOUSE	P01672 mus musculus
20	432	34.7	134	1	KV4C_HUMAN	P06314 homo sapien
21	428.5	34.4	109	1	KV3B_HUMAN	P01620 homo sapien
22	427.5	34.3	109	1	KV3D_HUMAN	P01622 homo sapien
23	427	34.3	111	1	KV3U_MOUSE	P01673 mus musculus
24	424	34.0	111	1	KV3C_MOUSE	P01656 mus musculus
25	424	34.0	115	1	KV3I_HUMAN	P04633 homo sapien
26	423.5	34.0	109	1	KV3E_HUMAN	P01623 homo sapien
27	423	33.9	112	1	KV3G_MOUSE	P01659 mus musculus
28	422.5	33.9	133	1	KV2F_HUMAN	P06310 homo sapien
29	421	33.8	111	1	KV3A_MOUSE	P01654 mus musculus
30	421	33.8	129	1	KV1W_HUMAN	P04431 homo sapien
31	416.5	33.4	133	1	KV4B_HUMAN	P06313 homo sapien
32	413.5	33.2	112	1	KV3B_MOUSE	P01655 mus musculus
33	412	33.1	111	1	KV3D_MOUSE	P03977 mus musculus

```

RL  HOPPE-SEYLER'S 2. Physiol. Chem. 348:1718-1722(1967).
RN  [7]
RP  SEQUENCE (BENCE-JONES PROTEIN AG).
RX  MEDLINE=69234734; PubMed=4893682;
RA  Titani K., Shinoda T., Putnam F.W.;
RT  "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT  complete sequence and the location of the disulfide bridges.";
RJ  J. Biol. Chem. 244:3550-3560(1969).
RN  [8]
RP  SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
RX  MEDLINE=70201507; PubMed=5447531;
RA  Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT  "Macroglobulin structure: variable sequence of light and heavy
RT  chains.";
RL  Science 169:56-59(1970).
CC  -1- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
CC  45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
CC  MARKER, 45-ALA AND 83-LEU.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC  -----
DR  EMBL; J00241; AAA58989.1; -
DR  EMBL; V00557; CAA23823.1; -
DR  PIR; A02116; K3HU.
DR  MIM; 147200; -
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003597; Ig_c1.
DR  Pfam; PF00047; Ig_1.
DR  SMART; SM00407; Igcl_1.
DR  PROSITE; PS00290; IG_MHC; 1.
KW  Immunoglobulin domain; Immunoglobulin C region.
FT  NON_TER 1
FT  DISULFID 26 86
FT  DISULFID 106 106
FT  VARIANT 83
FT  CONFLICT 14 14
FT  CONFLICT 57 57
FT  SEQUENCE 106 AA; 11609 MW; 51984D1FDD372CE8 CRC64;
SQ

```

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RP  SEQUENCE OF 1-35.
RX  MEDLINE=78235887; PubMed=98179;
RA  Burstein Y., Schechter I.;
RT  "Primary structures of N-terminal extra peptide segments linked to
RT  the variable and constant regions of immunoglobulin light chain
RT  precursors: implications on the organization and controlled
RT  expression of immunoglobulin genes.";
RJ  Biochemistry 17:2392-2400(1978).
RN  [2]
RP  SEQUENCE OF 21-131.
RX  MEDLINE=73140225; PubMed=4691517;
RA  McKean D.J., Potter M., Hood L.E.;
RT  "Mouse immunoglobulin chains. Pattern of sequence variation among
RT  kappa chains with limited sequence differences.";
RJ  Biochemistry 12:760-771(1973).
RN  [3]
RP  REVISIONS.
RX  MEDLINE=79012520; PubMed=99744;
RA  McKean D.J., Bell M., Potter M.;
RT  "Mechanisms of antibody diversity: multiple genes encode structurally
RT  related mouse kappa variable regions.";
RJ  Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
DR  PIR; A01935; KVM5M6.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; Ig_1.
DR  SMART; SM00406; Ig_v_1.
KW  Immunoglobulin V region; Signal.
FT  SIGNAL 1 20
FT  CHAIN 21 131
FT  DOMAIN 21 43
FT  DOMAIN 44 58
FT  DOMAIN 59 73
FT  DOMAIN 74 80
FT  DOMAIN 81 112
FT  DOMAIN 113 121
FT  DOMAIN 122 131
FT  DISULFID 43 112
FT  NON_TER 131 131
FT  SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;
SQ

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Query Match 44.0%; Score 548; DB 1; Length 131;
 Best Local Similarity 77.9%; Pred. No. 4.7e-38;
 Matches 102; Conservative 17; Mismatches 12; Indels 0; Gaps 0;

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QY 1 METDTILLVLLWVPGSTGDIVLTQSPGTLSPGGERATLSCAKSQSDVYDGSYMMWY 60
DB 1 METDTLLVLLWVPGSTGNIVLTQSPASLVSLGQRATISCRASESDVSYGNFMHWY 60
QY 61 QOKPGQAPRLIYVAAASNLSCIPDRFSGSGSTDTLTTHPVEEDATYYCQSNEDPR 120
DB 61 QOKPGQPKLLIYVAAASNLSCIPDRFSGSGSTDTLTIDPVEADDAATYYCQNNEDPW 120
QY 121 TFGQGTREIK 131
DB 121 TFGGGTKLEIK 131

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```

RESULT 3
KV3F_MOUSE STANDARD; PRT; 132 AA.
AC P01658;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION MOPC 321 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-37.

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QY 133 TVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 192
DB 1 TVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60
QY 193 KDTYLSLSLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 238
DB 61 KDTYLSLSLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 106

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RESULT 2
KV3I_MOUSE STANDARD; PRT; 131 AA.
AC P01661;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION MOPC 63 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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TX	MEDLINE=79073152; PubMed=103003;
RA	Weigert M., Gatmatan L., Loh E., Schilling J., Hood L.E.;
RT	"Rearrangement of genetic information may produce immunoglobulin
RL	diversity.";
RL	Nature 276:785-790(1978).
DR	PIR; E01937; KVM569.
DR	InterPro: IPR003006; Ig_MHC.
DR	InterPro: IPR003596; Ig_V.
DR	Pfam: PF00047; ig; 1.
DR	SMART; SM00406; IGv; 1.
KW	Immunoglobulin V region.
FT	DOMAIN 1 23
FT	DOMAIN 24 38
FT	DOMAIN 39 53
FT	DOMAIN 54 60
FT	DOMAIN 61 92
FT	DOMAIN 93 101
FT	DOMAIN 102 111
FT	DISULFID 23 92
FT	NON_TER 111 111
SQ	SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;
Query Match 40.9%; Score 510; DB 1; Length 111;	
Best Local Similarity 85.6%; Pred. No. 4.7e-35;	
Matches 95; Conservative 9; Mismatches 7; Indels 0; Gaps	
QY	21 DIVLTQSPGTLISLPSGERATLSKASQSDVYDGDGSYNMYQQKPQGAPRLIYAASNLES 80 : : : : :
Db	1 DIVLTQSPASLVSLGPQTATISCKASQSDVYDGDGSYNMYQQKGQPVKVLIPAAASNLES 60
QY	81 GDPFRSGSGSGDTFTLIHPVEEDAATYYCOOSNEDPRTFGGTGLEIK 131
Db	61 GPIPARFSGSGSGDTFTLIHPVEEDAATYYCOOSNEDPWTFGSGTKLEIK 111
RESULT 8	
ID	KV3L_MOUSE STANDARD; PRT; 111 AA.
AC	P01664;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	IG KAPPA CHAIN V-III REGION CBPC 101.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;	
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=79012520; PubMed=99744;
RA	McKen D.J., Bell M., Potter M.;
RT	"Mechanisms of antibody diversity: multiple genes encode structurally
RL	related mouse kappa variable regions.";
RT	Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC	-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR	PIR; A01936; KVMSC1.
DR	InterPro: IPR003006; Ig_MHC.
DR	InterPro: IPR003596; Ig_V.
DR	Pfam: PF00047; ig; 1.
DR	SMART; SM00406; IGv; 1.
KW	Immunoglobulin V region.
FT	DOMAIN 1 23
FT	DOMAIN 24 38
FT	DOMAIN 39 53
FT	DOMAIN 54 60
FT	DOMAIN 61 92
FT	DOMAIN 93 101
FT	DOMAIN 102 111
FT	DISULFID 23 92
FT	NON_TER 111 111
SQ	SEQUENCE 111 AA; 11964 MW; E2BIAD98AD965962 CRC64;


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Query Match          40.3%; Score 502; DB 1; Length 111;
Best Local Similarity 84.7%; Pred. No. 2.1e-34;
Matches 94; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 21 DIVLTQSPGTLSPGERATLSCASQSDVDGDSYNNWYQKPGQAPRLLIYAASNL 80
DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQONPGQPKLLIYAASNL 60

QY 81 GIPDRFSGSGGTFTLTITHPVEEDAATYYCQSNEDPRTFGGQTRLEIK 131
DB 61 GIPARFSGSGGTFTLTITHPVEEDAATYYCQSNEDPYTFGGGTRLEIK 111

RESULT 9
KV3L_HUMAN          STANDARD;          PRT;          129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DE 15-JUL-1999 (Rel. 38, Last sequence update)
DE IG KAPPA CHAIN V-III REGION HAH PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR; P0022; K3HUHA.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin v region; signal.
KW STGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match          40.2%; Score 500.5; DB 1; Length 129;
Best Local Similarity 74.2%; Pred. No. 3.3e-34;
Matches 98; Conservative 12; Mismatches 19; Indels 3; Gaps 1;

QY 1 METDTILLWLLVPGSGTGDIVLTQSPGTLSPGERATLSCASQSDVDGDSYNNWY 60
DB 1 METPAQLFLLLWLPDPTTGEIVLTQSPGTLSPGERATLSCASQSV---SSYLAWY 57

QY 61 QKQPGAPRLLIYAASNLGSGIPDRFSGSGGTFTLTITHPVEEDAATYYCQSNEDP 120
DB 58 QKQPGAPRLLIYGASSRATGIPDRFSGSGGTFTLTITISRLPEDEFAVYCCQYGTSPR 117

QY 121 TFGGQTRLEIKR 132
DB 118 TFGGQTRVEIKR 129

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RESULT 10
KV3P_MOUSE          STANDARD;          PRT;          110 AA.
AC P01688;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7210.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; D01937; KVM510.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin v region.
KW DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 100 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 101 110 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 110 110
SQ SEQUENCE 110 AA; 11950 MW; 69F1A5CE886B1249 CRC64;

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Query Match          39.5%; Score 492.5; DB 1; Length 110;
Best Local Similarity 84.7%; Pred. No. 1.2e-33;
Matches 94; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 21 DIVLTQSPGTLSPGERATLSCASQSDVDGDSYNNWYQKPGQAPRLLIYAASNL 80
DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQKPGQPKLLIYAASNL 60

QY 81 GIPDRFSGSGGTFTLTITHPVEEDAATYYCQSNEDPRTFGGQTRLEIK 131
DB 61 GIPARFSGSGGTFTLTITHPVEEDAATYYCQSNEDPYTFGGGTRLEIK 110

RESULT 11
KV3M_HUMAN          STANDARD;          PRT;          129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION HIC PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M

```

```
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR; PLO021; K3HUHI.
DR HSP; P01789; 2MCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 21 43 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 44 55 FRAMEWORK 2.
FT DOMAIN 56 70 FRAMEWORK 3.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match 39.1%; Score 487.5; DB 1; Length 129;
Best Local Similarity 72.7%; Pred. No. 3.8e-33;
Matches 96; Conservative 12; Mismatches 21; Indels 3; Gaps 1;

QY 1 METDTILLWLLVWPGSTGDIIVLTQSPGTLSPGERATLSCAKASQSVVDYDGSYMMWY 60
DB 1 METPAQLFLLLWLPDITGEIVLTQSPGTLSPGERATLSCAKASQSV---SSYLAWY 57

QY 61 QKPGQAPRLIIYAASNLSEIPDFSGSGGTDTLTIHPVEEEDAAITYCQSQNEEDPR 120
DB 58 QKPGQAPRLIIYGASSRATGIPDFSGSGGTDTLTIHPVEEEDAAITYCQSQNEEDPR 117

QY 121 TFGQGTREIKR 132
DB 118 TFGQGTREIKR 129

RESULT 12
KV3R_MOUSE STANDARD; PRT; 111 AA.
AC P01670;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG KAPPA CHAIN V-III REGION PC 6884.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE:
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR; A01938; KVM584.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
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FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12039 MW; 1E46988341858526 CRC64;

Query Match 36.4%; Score 454; DB 1; Length 111;
Best Local Similarity 77.5%; Pred. No. 1.7e-30;
Matches 86; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 21 DIVLTQSPGTLSPGERATLSCAKASQSVVDYDGSYMMWYQKPGQAPRLIIYAASNLSE 80
DB 1 DIVLTQSPGTLSPGERATLSCAKASQSVSGSYMMWYQKPGQAPRLIIYLASNLSE 60

QY 81 GIPDFSGSGGTDTLTIHPVEEEDAAITYCQSQNEEDPRTEGQGTREIKR 131
DB 61 GVPARFSGSGGTDTLTIHPVEEEDAAITYCQHSRELPRTEGSGTKLEIK 111

RESULT 13
KV3K_HUMAN STANDARD; PRT; 128 AA.
AC P06311;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE IG KAPPA CHAIN V-III REGION IARC/BL41 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobbeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
III.";
RL Nucleic Acids Res. 13:6499-6513(1985).
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CC -----
DR EMBL; Z00021; CAA77316.1; -
DR PIR; A01899; K3HU41.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 128 IG KAPPA CHAIN V-III REGION IARC/BL41.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 118 128 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;

Query Match 36.4%; Score 453; DB 1; Length 128;
Best Local Similarity 69.7%; Pred. No. 2.4e-30;
Matches 92; Conservative 13; Mismatches 23; Indels 4; Gaps 1;

QY 1 METDTILLWLLVWPGSTGDIIVLTQSPGTLSPGERATLSCAKASQSVVDYDGSYMMWY 60
DB 1 METPAQLFLLLWLPDITGEIVLTQSPGTLSPGERATLSCAKASQSV---SSNLAWY 56
```

Qy 61 QOKPQAPRLIYAASNLSEGIPDRFSGSGTDTLTTHPVEEADAATYYCQSNEDPR 120
Db 57 QOKRQSPRLIIRDASSRANGIPDRFSGSGTDTLTTHPVEEADAATYYCQSNEDPR 116
Qy 121 TFGGTRLEIKR 132
Db 117 TFGGTRLEIKR 128

RESULT 14
KV3H_MOUSE
ID KV3H_MOUSE STANDARD; PRT; 111 AA.
AC P01660;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 3741/TEPC 111.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (PC 3741).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatnaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
RN [2]
RP SEQUENCE (TEPC 111).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -1- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
DR PIR; A01934; KVM337.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;

Query Match 36.1%; Score 450; DB 1; Length 111;
Best Local Similarity 76.6%; Pred. No. 3.5e-30;
Matches 85; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

Qy 21 DIVLTQSPGTLSPGERATLSCAKASQSDYDGSYMNWYQKQPGAPRLIYAASNLSE 80
Db 1 DIVLTQSPASLAVSLGQRATISCRASESDYSGNSFMHWYQKQPGAPRLIYAASNLSE 60
Qy 81 GIPDRFSGSGTDTLTTHPVEEADAATYYCQSNEDPRTFGGTRLEIK 131
Db 61 GIPARFSGSGRTDTLTTHPVEEADAATYYCQSNEDPRTFGGTRLEIK 111

RESULT 15
KV3S_MOUSE
ID KV3S_MOUSE STANDARD; PRT; 111 AA.
AC P01671;
DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
OS IG KAPPA CHAIN V-III REGION PC 7175.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatnaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; B01938; KVM375.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12010 MW; F041E89AA7858523 CRC64;

Query Match 35.8%; Score 446; DB 1; Length 111;
Best Local Similarity 75.7%; Pred. No. 7.5e-30;
Matches 84; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

Qy 21 DIVLTQSPGTLSPGERATLSCAKASQSDYDGSYMNWYQKQPGAPRLIYAASNLSE 80
Db 1 DIVLTQSPASLAVSLGQRATISCRASKSVSTSGYSFMHWYQKQPGAPRLIYAASNLSE 60
Qy 81 GIPDRFSGSGTDTLTTHPVEEADAATYYCQSNEDPRTFGGTRLEIK 131
Db 61 GVPARFSGSGRTDTLTTHPVEEADAATYYCQSNEDPRTFGAGTKLEIK 111

Search completed: April 24, 2002, 15:13:45
Job time: 322 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 15:13:10 ; Search time 86.76 Seconds
(without alignments)
401.254 Million cell updates/sec

Title: US-09-499-662-52
Perfect score: 1246
Sequence: 1 METDTILLVLLWVPGSTG.....EVTHQGLSPVTKSFNRGEC 238
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_17:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	744.5	59.8	238	11 Q99M37	Q99M37 mus musculus
2	680	54.6	214	11 Q9RIA5	Q9RIA5 mus musculus
3	428.5	34.4	235	11 Q99M11	Q99M11 mus musculus
4	426.5	34.2	109	4 Q9UL78	Q9UL78 homo sapien
5	393.5	31.6	109	4 Q9UL86	Q9UL86 homo sapien
6	392	31.5	108	4 Q9UL77	Q9UL77 homo sapien
7	391	31.4	103	11 Q9JL80	Q9JL80 mus musculus
8	385	30.9	108	4 Q9UL79	Q9UL79 homo sapien
9	383	30.7	108	4 Q9UL70	Q9UL70 homo sapien
10	381	30.6	108	4 Q9UL83	Q9UL83 homo sapien
11	372.5	29.9	109	4 Q9UL85	Q9UL85 homo sapien
12	370.5	29.7	107	4 Q9UL81	Q9UL81 homo sapien
13	356	28.6	114	4 Q9UL80	Q9UL80 homo sapien
14	349.5	28.0	105	5 Q9U410	Q9U410 schistosoma
15	335	26.9	107	11 Q9ER29	Q9ER29 mus musculus
16	329	26.4	99	11 Q9JL74	Q9JL74 mus musculus
17	328	26.3	101	11 Q9JL78	Q9JL78 mus musculus
18	327	26.2	97	11 Q9JL76	Q9JL76 mus musculus
19	321.5	25.8	104	11 Q9JL82	Q9JL82 mus musculus

20	321	25.8	298	11 Q9YF0	Q9YF0 mus musculus
21	298	23.9	107	11 Q9JL84	Q9JL84 mus musculus
22	285	22.9	109	6 Q9N0W5	Q9N0W5 oryctolagus
23	246	19.7	107	4 Q9UL82	Q9UL82 homo sapien
24	234.5	18.8	107	4 Q9NSD6	Q9NSD6 homo sapien
25	229	18.4	130	4 Q9NP29	Q9NP29 homo sapien
26	225	18.1	130	11 Q9D8W4	Q9D8W4 mus musculus
27	200	16.1	484	11 Q99LA6	Q99LA6 mus musculus
28	198	15.9	267	13 Q90529	Q90529 ginglymosto
29	195.5	15.7	463	11 Q99LC4	Q99LC4 mus musculus
30	195	15.7	473	11 Q9D8L4	Q9D8L4 mus musculus
31	185.5	14.9	509	11 Q08907	Q08907 mus musculus
32	185.5	14.9	509	11 Q9QX57	Q9QX57 mus musculus
33	185.5	14.9	513	11 P97797	P97797 mus musculus
34	184.5	14.8	479	11 Q99M22	Q99M22 mus musculus
35	180.5	14.5	268	13 Q90524	Q90524 ginglymosto
36	179	14.4	361	4 Q9H1U5	Q9H1U5 homo sapien
37	178.5	14.3	468	11 Q99L31	Q99L31 mus musculus
38	178.5	14.3	506	6 Q46631	Q46631 bos taurus
39	174.5	14.0	509	11 Q9W7N4	Q9W7N4 mus musculus
40	174	14.0	105	11 Q99JC1	Q99JC1 mus musculus
41	174	14.0	398	4 Q00241	Q00241 homo sapien
42	173	13.9	473	11 Q99L25	Q99L25 mus musculus
43	172.5	13.8	509	11 P97710	P97710 rattus norv
44	172	13.8	372	4 Q9Y4V0	Q9Y4V0 homo sapien
45	171	13.7	252	13 Q90568	Q90568 ginglymosto

ALIGNMENTS

RESULT 1

Q99M37 PRELIMINARY; PRT; 238 AA.

AC Q99M37; 01-JUN-2001 (Tremblrel. 17, Created)

DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)

DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)

DB UNKNOWN (PROTEIN FORMGCG:5947).

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=MAMMARY TUMOR

RA	Strausberg R.;
RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BC02035; AA02035.1; -
SQ	SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 59.8%; Score 744.5; DB 11; Length 238;
Best Local Similarity 58.5%; Pred. No. 3.7e-61;
Matches 137; Conservative 41; Mismatches 55; Indels 1; Gaps 1;

Qy	6	ILLVLLWVPGSTGDIYLTOSPGTSLSPGERATLSCKASQSDY-DGDSYMNYYQOKP	64
Db	5	VRLVLMFWIPASSDDVVTQTPLSLPGLGQASISCRSSQSIIVHSNGNTILEVYLQKP	64
Qy	65	GOAPRLLIYAASNLGSGIPDRFSGSGSGTDFTLTHPVEEEDAATYYCQNSNDRPTFGQ	124
Db	65	GQSPKLLIYKSNRFGVDPDRFSGSGSGTDFTLKISRVAEDLGVYCFQGSHPVTFGS	124
Qy	125	GTRLEIKTVAAPSVTIFPPSDEQLKSGTASVCLLNNFYPREAKVQKVDNALSGNSQ	184
Db	125	GTLKLEIKRADAAPTYSIFPPSDEQLTSGGASVYCVCLNNFYPRKIDNVKWKIDGSRQNGV	184
Qy	185	ESVTEODSKDSTYSLSPTLTKSKADYKHKVYACEVTHOGLSSPTKSFNRGEC	238
Db	185	NSWTDQDQSKDSTYSNSPTLTKDYEYRHNSTYTCATHKTSPIVKSFNREK	238

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RESULT 2
Q9RIA5 PRELIMINARY; PRT; 214 AA.
AC Q9RIA5:
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Mista S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN
DR EMBL; AF152371; AAD40242.1; -.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; Ig; 1.
DR SMART; SM00410; Ig_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1 214
FT NON_TER 214 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 54.6%; Score 680; DB 11; Length 214;
Best Local Similarity 58.3%; Pred. No. 3.1e-55;
Matches 127; Conservative 34; Mismatches 53; Indels 4; Gaps 1;

Qy 21 DIVLTQSPGTLSPGERATLSCASQSDYDGDSDYNNWYQKPGQAPRLIIYAASNLES 80
Db 1 DIQQTQSPSYASLGERVTTICTKASQDI----NSYLSWFQKPGKSPKTIYRANRLVD 56
Qy 81 GIPDRFSGSGGTFTLTTHPVEEEDAATYYCQSNEDPRTFGGTRLEIKRTVAAPSVF 140
Db 57 GVPFRFSGSGGQDIYSLTISSELEWDGIYCYLQYDEFPFTFGSGTKLEIKRAADAPTVS 116
Qy 141 IFPPSDEQLKSTGASVSVCLLNFPYFPAKGVQKVDNALQSGNSQESVTEQDSKDSYSL 200
Db 117 IFPPSDEQLTSGGASVSVCLLNFPYFPAKGVQKVDNALQSGNSQESVTEQDSKDSYSL 176
Qy 201 STLTLRADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 177 STLTLTKDEYRHRNSYTCETAPHTKSTSPVIVCFNRNEC 214

RESULT 3
Q99M11 PRELIMINARY; PRT; 235 AA.
AC Q99M11:
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR WGC:5743).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002129; AAH02129.1; -.

Query Match 34.2%; Score 426.5; DB 4; Length 109;
Best Local Similarity 375.0%; Pred. No. 3.9e-32;
Matches 84; Conservative 8; Mismatches 17; Indels 3; Gaps 1;

Qy 21 DIVLTQSPGTLSPGERATLSCASQSDYDGDSDYNNWYQKPGQAPRLIIYAASNLES 80
Db 1 EIVLTQSPGTLSPGERATLSCASQSV---SSSYLAWYQKPGQAPRLIYGASSRAT 57
Qy 81 GIPDRFSGSGGTFTLTTHPVEEEDAATYYCQSNEDPRTFGGTRLEIKR 132
Db 58 GIPDRFSGSGGTFTLTISRLEPEDCAVYCYQYGGSSPLTFGGTKVEIKR 109

RESULT 5
Q9UL86 PRELIMINARY; PRT; 109 AA.
ID Q9UL86
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SQ SEQUENCE 235 AA; 25403 MW; 39807BFE6782A3FB CRC64;

Query Match 34.4%; Score 428.5; DB 11; Length 235;
Best Local Similarity 42.6%; Pred. No. 6.7e-32;
Matches 101; Conservative 36; Mismatches 87; Indels 13; Gaps 7;

Qy 7 LLWVLLWVPGSTGDIVLTQSPGTLSPGERATLSCASQSDYDGDSDYNNWYQKPGQ 66
Db 6 LLLVFLHLTGSCAQVLTQ--PSSVSTSLGSKTAKLPCKA--STGNIGSDYNNWYQYWG 62
Qy 67 APRLLIYAASNLESGIPDRFSGS--GSGTDFTLTHPVEEEDAATYYCQSNEDPRTFGQ 124
Db 63 SPTNNIYGDDLPSGVSDFSSIDSSNSAFLTIQNVAODEADYYCQSYSSGIRVFGG 122
Qy 125 GTRLEI-KRTVAAPSVFIFPPSDEQLKSGTASVCLLNFPYFPAKGVQKVDNALQSGNS 183
Db 123 GTKLTLSQPKTSPSYTLFPPSSELEETNKATLVCTISDFYPGVVTVDMKADG---TPVT 179
Qy 184 QESVTEQDSK--DSTYSLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 180 QGVETTPSKONNNKYMSSYLTLTAKAWETHSSYSCQVTHEG--HTVEKSLSRADC 234

RESULT 4
Q9UL78 PRELIMINARY; PRT; 109 AA.
ID Q9UL78
AC Q9UL78:
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN
DR EMBL; AF035036; AAD56272.1; -.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
FT NON_TER 1 109
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 34.2%; Score 426.5; DB 4; Length 109;
Best Local Similarity 375.0%; Pred. No. 3.9e-32;
Matches 84; Conservative 8; Mismatches 17; Indels 3; Gaps 1;

Qy 21 DIVLTQSPGTLSPGERATLSCASQSDYDGDSDYNNWYQKPGQAPRLIIYAASNLES 80
Db 1 EIVLTQSPGTLSPGERATLSCASQSV---SSSYLAWYQKPGQAPRLIYGASSRAT 57
Qy 81 GIPDRFSGSGGTFTLTTHPVEEEDAATYYCQSNEDPRTFGGTRLEIKR 132
Db 58 GIPDRFSGSGGTFTLTISRLEPEDCAVYCYQYGGSSPLTFGGTKVEIKR 109

RESULT 5
Q9UL86 PRELIMINARY; PRT; 109 AA.
ID Q9UL86
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AC Q9UL86;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DE 01-JUN-2001 (Tremblrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
CC EMBL; AF035028; AAD56264.1; -.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR003596; Iq_v.
DR Pfam; PF00047; Iq; 1.
DR SMART; SM00406; Iq; 1.
FT NON_TER 1
FT NON_TER 109
FT NON_TER 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 31.6%; Score 393.5; DB 4; Length 109;
Best Local Similarity 70.5%; Pred. No. 4.5e-29;
Matches 79; Conservative 9; Mismatches 21; Indels 3; Gaps 1;

QY 21 DIVLTQSPGTLSPGERATLSCASQSDVDGDSYNNWYQKQPGQAPRLIIYAASNLES 80
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 EVLTQSPGTLSPGERATLSCASQSV---SSYLAWYQKQPGQAPRLIIYGTSSRT 57

QY 81 GIPDRFSGSGGTFTLTTHPVEEDAATYYCQSNEDPRTFGGQTRLEIKR 132
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
58 GIPDRFSGSGSEDTLTITSLRLEDAFVYCYQYGSIFTFGPGTKVDIKR 109

RESULT 6
Q9UL77 PRELIMINARY; PRT; 108 AA.
ID Q9UL77 AC Q9UL77;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DE 01-JUN-2001 (Tremblrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
CC EMBL; AF035037; AAD56273.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR003596; Iq_v.
DR Pfam; PF00047; Iq; 1.
DR SMART; SM00406; Iq; 1.
FT NON_TER 1
FT NON_TER 108
FT NON_TER 108
```

```
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 31.5%; Score 392; DB 4; Length 108;
Best Local Similarity 66.1%; Pred. No. 6.1e-29;
Matches 74; Conservative 17; Mismatches 17; Indels 4; Gaps 1;

QY 21 DIVLTQSPGTLSPGERATLSCASQSDVDGDSYNNWYQKQPGQAPRLIIYAASNLES 80
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 DIQMTQSPSSLSASVGDRVTITCRASQSI---SSYLNWYQKPGKAPNLLIYAASSLOS 56

QY 81 GIPDRFSGSGGTFTLTTHPVEEDAATYYCQSNEDPRTFGGQTRLEIKR 132
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
57 GVPDRFSGSGGTFTLTITSLRLEDAFVYCYQYGSIFTFGPGTKVEIKR 108

RESULT 7
Q9UL80 PRELIMINARY; PRT; 103 AA.
ID Q9UL80 AC Q9UL80;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
CC EMBL; AF206026; AAF69324.1; -.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR003596; Iq_v.
DR Pfam; PF00047; Iq; 1.
DR SMART; SM00406; Iq; 1.
FT NON_TER 1
FT NON_TER 103
FT NON_TER 103
SQ SEQUENCE 103 AA; 11224 MW; EC87D653DB3AAB21 CRC64;

Query Match 31.4%; Score 391; DB 11; Length 103;
Best Local Similarity 70.6%; Pred. No. 7.1e-29;
Matches 72; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 30 TSLSPGERATLSCASQSDVDGDSYNNWYQKQPGQAPRLIIYAASNLES 89
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2 SLAVSLGQRAITSCRASEVEYGTSLMQYQKPGQPKLLIYAASNVESGVPARFSGS 61

QY 90 GSGTDFTLTIHPVEEDAATYYCQSNEDPRTFGGQTRLEIK 131
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
62 GSGTDFSLNIHPVEEDDIAMFYCQSRKVPWTFGGGTLEIK 103

RESULT 8
Q9UL79 PRELIMINARY; PRT; 108 AA.
ID Q9UL79 AC Q9UL79;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
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RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035035; AAD56271.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 30.9%; Score 385; DB 4; Length 108;
Best Local Similarity 66.1%; Pred. No. 2.7e-28;
Matches 74; Conservative 13; Mismatches 21; Indels 4; Gaps 1;

Qy 21 DIVLTQSPGTLSPGERATLSCASQSDYDGDSDYNNYQKPGQAPRLIIYAASNL 80
Db 1 DIVMTQSPSSLSASTGDRVTISCRMSQGI-----SSYLAWYQKPKGKAPPELLIIYAASLTQS 56

Qy 81 GIPDRFSGSGGTDFLTTHHPVEEDAATYYCQSQNEDPRFTGQGRLEIKR 132
Db 57 GVPFRSGSGGTDFLTTHHPVEEDAATYYCQSQNEDPRFTGQGRLEIKR 108

RESULT 9
Q9UL70
ID Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035044; AAD56280.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 30.7%; Score 383; DB 4; Length 108;
Best Local Similarity 63.4%; Pred. No. 4.1e-28;
Matches 71; Conservative 17; Mismatches 20; Indels 4; Gaps 1;

Qy 21 DIVLTQSPGTLSPGERATLSCASQSDYDGDSDYNNYQKPGQAPRLIIYAASNL 80
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGI-----SNYLAWYQKPKGKAPPELLIIYAASLTQS 56

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Qy 81 GIPDRFSGSGGTDFLTTHHPVEEDAATYYCQSQNEDPRFTGQGRLEIKR 132
Db 57 GVPFRSGSGGTDFLTTHHPVEEDAATYYCQSQNEDPRFTGQGRLEIKR 108

RESULT 10
Q9UL83
ID Q9UL83 PRELIMINARY; PRT; 108 AA.
AC Q9UL83;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035031; AAD56267.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 30.6%; Score 381; DB 4; Length 108;
Best Local Similarity 67.9%; Pred. No. 6.3e-28;
Matches 76; Conservative 12; Mismatches 20; Indels 4; Gaps 1;

Qy 21 DIVLTQSPGTLSPGERATLSCASQSDYDGDSDYNNYQKPGQAPRLIIYAASNL 80
Db 1 EIVMTQSPATLSVSPGERATLSCASQSV-----SSNLAWYQKPKGQAPRLIIYCASTRAT 56

Qy 81 GIPDRFSGSGGTDFLTTHHPVEEDAATYYCQSQNEDPRFTGQGRLEIKR 132
Db 57 GIPARFSGSGGTDFLTTHHPVEEDAATYYCQSQNEDPRFTGQGRLEIKR 108

RESULT 11
Q9UL85
ID Q9UL85 PRELIMINARY; PRT; 109 AA.
AC Q9UL85;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX

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Job time: 288 sec

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FT NON_TER 106 106
SQ SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;

Query Match      28.0%; Score 349.5; DB 5; Length 106;
Best Local Similarity 62.4%; Pred. No. 5.1e-25;
Matches 68; Conservative 13; Mismatches 23; Indels 5; Gaps 1;

Qy 23 VLTQSPGTLSPGGERATLSCAKSQSV--DYDGDSDYMNWYQKPGQAPRLIIYAASNLESGI 82
    :||||| :| ||||| :| :| ||| :| :| ||||| ||||| ||| |||
Db 3  LLTQSPAIMSASPGKVTMTCSASSV-----SYVYWLQKPGSSPRLLIYDTNLSASGV 57

Qy 83 PDRFSGSGGTDFTLTTHPVEEEDAATYYCQSNEDPRTFGQTRLEIK 131
    | ||||| ||| :||| :| ||||| ||| ||| ||| |||
Db 58 PVRFSGSGGTSYSLTISRMEADAATYYCQWTSYPFTFGSGTKLEK 106

RESULT 15
Q9ERZ9          PRELIMINARY;      PRT;    107 AA.
AC Q9ERZ9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;
RT "Cloning and sequencing of the light chain fragment of variable region
RL genes of an anti-hTNF-a monoclonal antibody.";
RL J. Cell. Mol. Immunol. 12:21-26(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT "Construction and sequencing of the single-chain antibody gene of a
RL human TNF-alpha specific monoclonal antibody.";
RL T1 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
    DOMAIN
DR EMBL; AF262753; AAC23804.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00406; IGv; 1.
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11784 MW; 2B15EEA6604A26C3 CRC64;

Query Match      26.9%; Score 335; DB 11; Length 107;
Best Local Similarity 58.9%; Pred. No. 1.1e-23;
Matches 63; Conservative 17; Mismatches 25; Indels 2; Gaps 1;

Qy 24 LTQSPGTLSPGGERATLSCAKSQSV--DYDGDSDYMNWYQKPGQAPRLIIYAASNLESG 81
    :||||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 1  MTQSPSSLSAMSGVKVTMSCKSSQSVLSNTQKNLAWYQKKPGQSPPELLLYFASTRESG 60

Qy 82 IPDRFSGSGGTDFTLTTHPVEEEDAATYYCQSNEDPRTFGQTRL 128
    :||||| ||||| ||||| :| :| :| :| :| :| :| :| :| :| :| :|
Db 61 VPDRFMGSGGTDFTLTITSSVQTEDLADYFCQHQHYRTPFTFGSGTKL 107

Search completed: April 24, 2002, 15:13:10
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 15:09:52 ; Search time 85.18 Seconds
(without alignments)
206.967 Million cell updates/sec

Title: US-09-499-662-54

Perfect score: 1249

Sequence: 1 METDRIILLWLLVLPVSTG.....EVTHQGLSPVTKSPNRGEC 238

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_1101:*

1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT:*

2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT:*

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22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1249	100.0	238	AAW83033	Anti-Fas humanised
2	1249	100.0	238	AAW83033	Humanised anti-Fas
3	1249	100.0	238	AAW83033	Humanised anti-Fas
4	1238	99.1	238	AAW83032	Anti-Fas humanised
5	1238	99.1	238	AAW83032	Humanised anti-Fas
6	1238	99.1	238	AAW83032	Humanised anti-Fas
7	1231	98.6	238	AAW83035	Anti-Fas humanised
8	1231	98.6	238	AAW83035	Humanised anti-Fas
9	1231	98.6	238	AAW83031	Humanised anti-Fas
10	1194	95.6	238	AAW83031	Humanised anti-Fas
11	1194	95.6	238	AAW83031	Humanised anti-Fas

12	1194	95.6	238	21	AAW83033	Humanised anti-Fas
13	1193	95.5	238	19	AAW83034	Anti-Fas humanised
14	1193	95.5	238	21	AAW83034	Humanised anti-Fas
15	1193	95.5	238	21	AAW83034	Humanised anti-Fas
16	1193	95.5	238	21	AAW83034	Humanised anti-Fas
17	1154	92.4	238	21	AAW83032	Humanised anti-Fas
18	1153	92.3	238	21	AAW83032	Humanised anti-Fas
19	1039	83.2	240	20	AAW50161	Humanised anti-Fas
20	1030	82.5	218	18	AAW13563	Humanised anti-Fas
21	1024.5	82.0	235	21	AAW93702	The kappa chain of
22	1024.5	82.0	235	21	AAW93729	The kappa chain of
23	1021	81.7	234	21	AAW92239	Human bone marrow
24	1018	81.5	237	20	AAW73873	Human antitc epsil
25	1016	81.3	218	20	AAW95658	Mus musculus anti-
26	1016	81.3	218	21	AAW95200	Light chain amino
27	1016	81.3	218	22	AAW76947	Full variable ligh
28	1012	81.0	240	20	AAW73875	Human antitc epsil
29	1010	80.9	234	21	AAW93708	The kappa chain of
30	1010	80.9	234	21	AAW93733	The kappa chain of
31	1009	80.8	218	14	AAW33312	Humanised MaElI Ve
32	1007.5	80.7	233	21	AAW93704	The kappa chain of
33	1007.5	80.7	233	21	AAW93731	The kappa chain of
34	993	79.5	218	20	AAW50030	Human E27 anti-IgE
35	993	79.5	218	20	AAW95660	Mus musculus anti-
36	993	79.5	218	20	AAW95662	Mus musculus anti-
37	993	79.5	218	21	AAW7472	Amino acid sequenc
38	993	79.5	218	22	AAW74211	E27 anti-IgE antib
39	992	79.4	236	22	AAW71272	Human gene 2-encod
40	992	79.4	240	22	AAW00815	Human Immunoglobul
41	990	79.3	218	20	AAW95669	Mus musculus anti-
42	990	79.3	218	20	AAW95664	Mus musculus anti-
43	990	79.3	218	22	AAW47087	Anti-IgE antibody,
44	990	79.3	218	22	AAW76949	Full length light
45	990	79.3	218	22	AAW76951	Full length light

ALIGNMENTS

RESULT 1

AAW83033

ID AAW83033 standard; Protein: 238 AA.

XX AC AAW83033;

XX AC AAW83033;

DT 15-MAR-1999 (first entry)

XX DE Anti-Fas humanised antibody HFE7A light chain MM type.

XX DE HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;

KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;

KW systemic lupus erythematosus; graft versus host disease;

KW Sjogren syndrome; pernicious anaemia; Addison's disease;

KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;

KW rheumatoid arthritis; autoimmune haemolytic anaemia;

KW myasthenia gravis; multiple sclerosis; Basedow's disease;

KW thrombopenia purpura; insulin-dependent diabetes; allergy;

KW atopy; arteriosclerosis; myocarditis; cardiomyopathy; AIDS;

KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;

KW transplant rejection; therapy.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Peptide 1..20

FT Protein 21..238

FT Region 21..131

FT Region 132..238

FT /label= Variable

FT /label= Constant

FT Region 44...58
 FT /label= CDR_L1
 FT /note= "claim 9"
 FT 74..80
 FT /label= CDR_L2
 FT /note= "claim 9"
 FT 113..121
 FT /label= CDR_L3
 FT /note= "claim 9"
 XX
 XX
 PN AU9859701-A.
 XX
 XX 08-OCT-1998.
 XX
 XX 30-MAR-1998; 98AU-0059701.
 XX
 XX 08-OCT-1997; 97JP-0276064.
 PR 01-APR-1997; 97JP-0082953.
 PR 25-JUN-1997; 97JP-0169088.
 XX
 XX (SANY) SANKYO CO LTD.
 XX
 XX Akio S. Hideyuki H., Hiroko Y., Jun O., Kimihisa I;
 PI Masahiko O., Nobufusa S., Shin Y., Tohru T;
 XX
 XX WPI: 1998-543440/47.
 DR N-PSDB; AAV70076.
 XX
 XX New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX
 XX Claim 21; Page 202; 292pp; English.
 PS
 XX This is the amino acid sequence of the MM type humanised light
 CC chain of murine anti-human Fas monoclonal antibody HFE7A. E. coli
 CC SANK 73697 harbors plasmid pSHGM6 carrying a fusion fragment of the
 CC humanised MM type HFE7A light chain and DNA encoding the region of
 CC human kappa chain, and is deposited as FERM BP-6071 (claimed). The
 CC invention provides methods for producing humanised antibodies by
 CC culturing host cells. Humanised versions of HFE7A (see AAM83031-37),
 CC like native HFE7A, are capable of inducing apoptosis in abnormal
 CC cells expressing Fas, and of inhibiting Fas-induced apoptosis in
 CC normal cells. The humanised antibodies are used to evaluate, in
 CC animal models, treatments of diseases that involve Fas/Fas ligand
 CC interactions, and also to treat such diseases, including autoimmune
 CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
 CC graft versus host disease, Sjogren syndrome, pernicious anaemia,
 CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
 CC sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
 CC thrombopenia purpura and insulin-dependent diabetes), allergies,
 CC atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
 CC nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
 CC rejection (all claimed).
 XX
 XX Sequence 238 AA;
 SQ
 Query Match 100.0%; Score 1249; DB 19; Length 238;
 Best Local Similarity 100.0%; Pred. No. 1.2e-65;
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 METDTILLWLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCAKASQSDVDGDSYNNWY 60
 Db 1 metdtillwllwvpgstgdivltqspgtlspsgeratlsckasqsdvdgdsynnwy 60
 QY 61 QOKFGCPKLLIYAASNLGSGIPRFGSGSGTDTLTILHPVEEEDATYCCQSNEDPR 120
 Db 61 qkfgcpklliyasnlsgiprfgsgsgtdtltihpveeedatyyccqsgnedpr 120
 QY 121 TFGGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCVCLNNFYPREAKVQWKVDNALQ 180

Db 121 tfggtrleikrtvaapsvfifppsqdeqlksgtasvvcvclnnfypreakvqwkvdnalqs 180
 QY 181 GNSQSVTEQDSKDSYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNREGC 238
 Db 181 gnsqsvteqdsksdyslsstltlskadyekhkyacevthqgisspvtksfnrgec 238
 RESULT 2
 AAB14774
 ID AAB14774 standard; Protein; 238 AA.
 XX
 XX AC AAB14774;
 XX
 XX 24-NOV-2000 (first entry)
 XX
 XX Humanised anti-Fas antibody light chain, SEQ ID NO:54.
 DE
 DE Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; humanised antibody; complementarity determining region; CDR;
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
 KW hepatitis; AIDS; graft rejection; light chain.
 XX
 XX Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX
 XX JP2000169393-A.
 PN
 XX 20-JUN-2000.
 PD
 XX
 PF 30-SEP-1999; 99JP-0278301.
 XX
 XX 30-SEP-1998; 98JP-0276883.
 PR
 XX (SANY) SANKYO CO LTD.
 PA
 XX WPI: 2000-485645/43.
 DR N-PSDB; AAA72126.
 XX
 XX Preventive or treating agent for the diseases caused by an abnormality
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody
 XX
 XX Claim 20; Page 83; 139pp; Japanese.
 PS
 XX The invention relates to compositions for the prevention or treatment
 CC of diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The compositions of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
 CC represent the light chains of several humanised HFE7A-derived anti-Fas
 CC antibodies.
 XX
 XX Sequence 238 AA;
 SQ
 Query Match 100.0%; Score 1249; DB 21; Length 238;
 Best Local Similarity 100.0%; Pred. No. 1.2e-65;
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 METDTILLWLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCAKASQSDVDGDSYNNWY 60
 Db 1 metdtillwllwvpgstgdivltqspgtlspsgeratlsckasqsdvdgdsynnwy 60

QY 61 QOKPQPKLLIYAASNLGSGIPDRFSGSGSGTDFTLTIHPVEEDAAATYYCQOSNEDPR 120
 Db 61 qkpgqpkllyaaanslesgipdrfsgsgsgtdftltihpveeedaatyyccqgsnedpr 120
 QY 121 TFGGTRLEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQS 180
 Db 121 tfggtrleikrtvaapsvfiFFPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQS 180
 QY 181 GNSQESYTEODSKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 Db 181 gnsqesvteqdsksdstyslslstltlskadyekhkvyacevthqglsspvtksfnrgec 238

RESULT 3
 AAW90924
 ID AAW90924 standard; Protein: 238 AA.
 XX
 AC AAW90924;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Humanised anti-Fas antibody HFE7A light chain MM type protein.
 XX
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; anti-rheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX
 OS Synthetic.
 XX
 PN EP990663-A2.
 XX
 PD 05-APR-2000.
 XX
 PF 29-SEP-1999; 99EP-0307711.
 XX
 PR 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX
 XX (SANY) SANKYO CO LTD.
 XX
 PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX
 DR WPI; 2000-258930/23.
 DR N-PSDB; AAA11564.
 XX
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems
 XX
 PS Example reference 14; Page 119-120; 263pp; English.
 XX
 CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC anti-rheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic

CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A light chain MM type which is used in
 CC the method described in the invention.
 XX
 SQ Sequence 238 AA;

Query Match 100.0%; Score 1249; DB 21; Length 238;
 Best Local Similarity 100.0%; Pred. NO. 1.2e-65;
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METDTILLWLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCAKASQSVYDGDSYMNY 60
 Db 1 metdtillwllwvpgstgdivltqspgtlsispggeratlsckasqsvdygdSYMNY 60
 QY 61 QOKPQPKLLIYAASNLGSGIPDRFSGSGSGTDFTLTIHPVEEDAAATYYCQOSNEDPR 120
 Db 61 qkpgqpkllyaaanslesgipdrfsgsgsgtdftltihpveeedaatyyccqgsnedpr 120
 QY 121 TFGGTRLEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQS 180
 Db 121 tfggtrleikrtvaapsvfiFFPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQS 180
 QY 181 GNSQESYTEODSKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 Db 181 gnsqesvteqdsksdstyslslstltlskadyekhkvyacevthqglsspvtksfnrgec 238

RESULT 4
 AAW83032
 ID AAW83032 standard; Protein: 238 AA.
 XX
 AC AAW83032;
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE Anti-Fas humanised antibody HFE7A light chain HM type.
 XX
 KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjorgen syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..120
 FT /label= Sig_peptide
 FT Protein 21..238
 FT /label= Mat_protein
 FT Region 21..131
 FT /label= Variable
 FT Region 132..238
 FT /label= Constant
 FT Region 44..58

Db 1 metdtillwllwpgstgdivltsgpdlsgpgeratlscasqsdvdydgsymwy 60
 QY 61 QQRPGOPPKLLIYAASNLGSIPIPRFSGSGSGTDFTLTIHPVEEEDAAATYCCQSNEDPR 120
 Db 61 qkpgqpapriliyaasnlsgipdrfsgsgsgtdftlthpveedaatyccqsgnedpr 120
 QY 121 TFGGGRLEIKRVAAPSVFIPFPPSDQSLKSGTASVCLNNFYPRAKVQWKVDNALQS 180
 Db 121 tfgggrtleikrvaapsvfippsdeqlksgtasvclnnfypreakvqwkvdnalqs 180
 QY 181 GNSQSVTEODSKDSTYSLSTLTLSKADYKHKVYACEVTHOGLSPVTKSNRGE 238
 Db 181 gnsqsvteqsdksdstyslslstltlskadyekhkvyacevthglspsvtksnrg 238
 RESULT 6
 ID AAW90923 standard; Protein; 238 AA.
 XX
 AC AAW90923;
 DT 08-AUG-2000 (first entry)
 XX
 DE Humanised anti-Fas antibody HFE7A light chain HM type protein.
 XX
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatocytic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX
 OS Synthetic.
 XX
 EP990663-A2.
 XX
 PD 05-APR-2000.
 XX
 PF 29-SEP-1999; 99EP-0307711.
 XX
 PR 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 PI WPI: 2000-258930/23.
 DR N-PSDB; AAIL563.
 XX
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems
 XX
 PS Example reference 14; Page 117-118; 263pp; English.
 XX
 CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent

CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Sjogren's syndrome, pernicious or hypoplastic
 CC versus host disease, Crohn's disease, Goodpasture syndrome, Crohn's
 CC anemia, Addison's disease, scleroderma, sterility, myasthenia gravis,
 CC disease, autoimmune hemolytic anemia, thrombopenia purpura, insulin
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A light chain HM type which is used in
 CC the method described in the invention.
 XX
 SQ Sequence 238 AA;

Query Match 99.1%; Score 1238; DB 21; Length 238;
 Best Local Similarity 99.2%; Pred. No. 5.2e-65;
 Matches 236; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 METDTILLWLLWPGSTGDIVLTQSPGTLISLSPGERATLSCASQSDVDYDGSYNNWY 60
 Db 1 metdtillwllwpgstgdivltqspgtlslspgeratlscasqsdvdydgsymwy 60
 QY 61 QQRPGOPPKLLIYAASNLGSIPIPRFSGSGSGTDFTLTIHPVEEEDAAATYCCQSNEDPR 120
 Db 61 qkpgqpapriliyaasnlsgipdrfsgsgsgtdftlthpveedaatyccqsgnedpr 120
 QY 121 TFGGGRLEIKRVAAPSVFIPFPPSDQSLKSGTASVCLNNFYPRAKVQWKVDNALQS 180
 Db 121 tfgggrtleikrvaapsvfippsdeqlksgtasvclnnfypreakvqwkvdnalqs 180
 QY 181 GNSQSVTEODSKDSTYSLSTLTLSKADYKHKVYACEVTHOGLSPVTKSNRGE 238
 Db 181 gnsqsvteqsdksdstyslslstltlskadyekhkvyacevthglspsvtksnrg 238

RESULT 7
 AAW83035
 ID AAW83035 standard; Protein; 238 AA.
 XX
 AC AAW83035;
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE Anti-Fas humanised antibody HFE7A light chain PDHM type.
 XX
 KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT Protein 21..238
 FT Region 21..231
 FT /label= Sig_peptide
 FT /label= Mat_protein
 FT /label= Variable

FT Region /label= Mat_protein
 FT 21..131
 FT /label= Variable
 FT 132..238
 FT /label= Constant
 FT 44..58
 FT /label= CDR_L1
 FT /note= "claim 9"
 FT 74..80
 FT /label= CDR_L2
 FT /note= "claim 9"
 FT 113..121
 FT /label= CDR_L3
 FT /note= "claim 9"
 PN AU9859701-A.
 PD 08-OCT-1998.
 XX 30-MAR-1998; 98AU-0059701.
 XX 08-OCT-1997; 97JP-0276064.
 PR 01-APR-1997; 97JP-0082953.
 PR 23-JUN-1997; 97JP-0169088.
 XX (SANY) SANKYO CO LTD.
 PA Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX WPI: 1998-543440/47.
 DR N-PSDB; AAV70074.
 XX New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX Claim 21; Page 199-199; 292pp; English.
 PS This is the amino acid sequence of the HH type humanised light
 XX chain of murine anti-human Fas monoclonal antibody HFE7A.
 CC Humanisation of the murine sequence (see AAW83042) entailed making
 CC P47A, K49R, H80S, P81R, V82L, E84P, E85A, A87F and T89V amino acid
 CC substitutions; these residues are conserved in the human light
 CC chain (kappa chain). Host cell Escherichia coli pHSCH7 SANK 73497
 CC harbors plasmid pHSCH7 carrying a fusion fragment of the humanised
 CC HH type HFE7A light chain and DNA encoding the region of human
 CC immunoglobulin kappa chain, and is deposited as FERM BP-6073
 CC (claimed). The invention provides methods for producing humanised
 CC antibodies by culturing host cells. Humanised versions of HFE7A
 CC (see AAW83031-37), like native HFE7A, are capable of inducing
 CC apoptosis in abnormal cells expressing Fas, and of inhibiting
 CC Fas-induced apoptosis in normal cells. The humanised antibodies
 CC are used to evaluate, in animal models, treatments of diseases that
 CC involve Fas/Fas ligand interactions, and also to treat such
 CC diseases, including autoimmune disease (e.g. systemic lupus
 CC erythematosus, Hashimoto's disease, graft versus host disease,
 CC Sjogren syndrome, pernicious anaemia, Addison's disease,
 CC scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid
 CC arthritis, autoimmune haemolytic anaemia, sterility, myasthenia
 CC gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura
 CC and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
 XX Sequence 238 AA;

Query Match 95.6%; Score 1194; DB 19; Length 238;
 Best Local Similarity 96.2%; Pred. No. 1.8e-62;
 Matches 229; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 METDTILLWLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCASQSDVYDGSYMMWY 60
 DQ 1 metdtillwllwvpgstgdivltqspgtlspsgeratlsckasgsdvydgdsymmwy 60
 QY 61 QOKPGQPKLLIYAASNLSCGIPDRFSGSGSGTFTLTTHPVEEDATYYCQGSNEDPR 120
 DQ 61 qkpgqpklliyaaanlesgipdrfsgsgsgtdftltthpveedatyyccqgsnedpr 120
 QY 121 TFGGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
 DQ 121 tfggtrleikrtvaapsvfifpppsdeqlksgtasvvcllnnfypreakvqwkvdnalqs 180
 QY 181 GNSQSVTEQDSKDSYSLSTLTSLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 DQ 181 gnsqsvteqdsksdyslsstltslskadyekhkvyacevthqglsspvtksfnrgec 238
 RESULT 11
 AAB14772
 ID AAB14772 standard; Protein; 238 AA.
 XX
 AC AAB14772;
 XX
 DT 24-NOV-2000 (first entry)
 XX
 DE Humanised anti-Fas antibody light chain, SEQ ID NO:50.
 XX
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; humanised antibody; complementarity determining region; CDR;
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
 KW hepatitis; AIDS; graft rejection; light chain.
 XX
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX
 PN JP2000169393-A.
 PD 20-JUN-2000.
 XX
 PF 30-SEP-1999; 99JP-0278301.
 XX
 PR 30-SEP-1998; 98JP-0276883.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 DR WPI: 2000-485645/43;
 DR N-PSDB; AAA72124.
 XX
 PT Preventive or treating agent for the diseases caused by an abnormality
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody
 XX
 PS Claim 20; Page 78-79; 139pp; Japanese.
 XX
 CC The invention relates to compositions for the prevention or treatment
 CC of diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The composition of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
 CC represent the light chains of several humanised HFE7A-derived anti-Fas
 CC antibodies.
 XX Sequence 238 AA;

Query Match 95.6%; Score 1194; DB 21; Length 238;
Best Local Similarity 96.2%; Pred. No. 1.8e-62;
Matches 229; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 METDTILLWVLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSDVDGDSYMNWY 60
Db 1 metdtillwvllwvpgstgdivltqspgtlsispggeratlsckasqsdvdgdsymw 60

QY 61 OOKPQPKLLIYAASNLSEGIPIRFSGSGTDTLTIHPVEEDAATYYCQSNEDPR 120
Db 61 qkqpgqaprllyaaasnlsegiipdrfsqsgtdtltihpveedaatyycqsnedpr 120

QY 121 TFGQTRLEIKRTVAAPSFFIPPSDEQLKSGTASVCLLNFFYPREAKVQKVDNALQS 180
Db 121 tfgqgtrleikrtvaapsffippsdeqlksgtasvcllnffypreakvqkvdnalqs 180

QY 181 GNSQSVTEQDSKSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNREGC 238
Db 181 gnsqsvteqdsksdtsylstltlskadyekhkyacevthqglsspvtksfnregc 238

RESULT 12
AAW90922
ID AAW90922 standard; Protein; 238 AA.
XX
AC AAW90922;
XX
DT 08-AUG-2000 (first entry)
XX

Humanised anti-Fas antibody HFE7A light chain HH type protein.
DE Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX Synthetic.
XX
XX EP990663-A2.
XX
XX 05-APR-2000.
XX
XX 29-SEP-1999; 99EP-0307711.
XX
XX 30-SEP-1998; 98JP-0276881.
XX
XX 30-SEP-1998; 98JP-0276882.
XX
XX (SANY) SANKYO CO LTD.
XX
XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX
XX WPI: 2000-258930/23.
XX
XX N-PSDB; AAA11562.
XX
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
XX inflammatory or autoimmune disease, induces apoptosis selectively in
XX cells with abnormal Fas-Fas ligand systems
XX
XX Example reference 14; Page 114-115; 263pp; English.
XX
XX This invention describes a novel humanized anti-Fas antibody-like
XX molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
XX ligand system, by binding to Fas on the cell surface, and prevents
XX apoptosis in cells with a normal system, by inhibiting binding between
XX Fas and its ligand. The products of the invention have anti-inflammatory,

anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
immunomodulatory, dermatological, immunosuppressive, antirheumatic,
antirheumatic, nephrotropic, antiinfertility, neuroprotective,
antiarteriosclerotic, cardiac and hepatropic activity. (I) induce
apoptosis by binding to cell surface Fas or inhibit it by competitive
inhibition of ligand binding. (I) are used to treat and/or prevent
diseases associated with the Fas/Fas ligand system, especially systemic
lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
(B, C or D) or alcoholic), and transplant rejection. (I) selectively
inhibit apoptosis in normal cells but selectively induce it in abnormal
cells. They bind to both human and murine Fas, so can be evaluated in
murine disease models. (I) act on the active site of Fas, i.e. they mimic
the native ligand, do not induce liver disease, and have reduced risk of
inducing a human anti-murine antibody response. This sequence represents
a humanised anti-Fas antibody HFE7A light chain HH type which is used in
the method described in the invention.

XX
SQ Sequence 238 AA;

Query Match 95.6%; Score 1194; DB 21; Length 238;
Best Local Similarity 96.2%; Pred. No. 1.8e-62;
Matches 229; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 METDTILLWVLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSDVDGDSYMNWY 60
Db 1 metdtillwvllwvpgstgdivltqspgtlsispggeratlsckasqsdvdgdsymw 60

QY 61 OOKPQPKLLIYAASNLSEGIPIRFSGSGTDTLTIHPVEEDAATYYCQSNEDPR 120
Db 61 qkqpgqaprllyaaasnlsegiipdrfsqsgtdtltihpveedaatyycqsnedpr 120

QY 121 TFGQTRLEIKRTVAAPSFFIPPSDEQLKSGTASVCLLNFFYPREAKVQKVDNALQS 180
Db 121 tfgqgtrleikrtvaapsffippsdeqlksgtasvcllnffypreakvqkvdnalqs 180

QY 181 GNSQSVTEQDSKSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNREGC 238
Db 181 gnsqsvteqdsksdtsylstltlskadyekhkyacevthqglsspvtksfnregc 238

RESULT 13
AAW83034
ID AAW83034 standard; Protein; 238 AA.
XX
AC AAW83034;
XX
DT 15-MAR-1999 (first entry)
XX
XX Anti-Fas humanised antibody HFE7A light chain PDHH type.
XX
XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
XX apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
XX systemic lupus erythematosus; graft versus host disease;
XX Sjogren syndrome; pernicious anaemia; Addison's disease;
XX scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
XX rheumatoid arthritis; autoimmune haemolytic anaemia;
XX myasthenia gravis; multiple sclerosis; Basedow's disease;
XX thrombopenia purpura; insulin-dependent diabetes; allergy;
XX atopy; arteriosclerosis; myocarditis; cardiomyopathy;
XX glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
XX transplant rejection; therapy.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH

FT Peptide 1..20
 FT /label= Sig_peptide
 FT Protein 21..238
 FT /label= Mat_protein
 FT Region 21..131
 FT /label= Variable
 FT Region 132..238
 FT /label= Constant
 FT Region 44..58
 FT /label= CDR_L1
 FT /note= "claim 9"
 FT Region 74..80
 FT /label= CDR_L2
 FT /note= "claim 9"
 FT Region 113..121
 FT /label= CDR_L3
 FT /note= "claim 9"
 XX
 PN AU9859701-A.
 XX
 PD 08-OCT-1998.
 XX
 PF 30-MAR-1998; 98AU-0059701.
 XX
 PR 08-OCT-1997; 97JP-0276064.
 PR 01-APR-1997; 97JP-0082953.
 PR 25-JUN-1997; 97JP-0169088.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 PI Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX
 DR WPI: 1998-543440/47.
 DR N-PSDB; AAV70077.
 XX
 PT New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX
 PS Claim 21; Page 218; 292pp; English.
 XX
 CC This is the amino acid sequence of the PDHH type humanised light
 CC chain of murine anti-human Fas monoclonal antibody HFE7A.
 CC Humanisation of the murine sequence (see AAW83042) entailed making
 CC DLE, P47A, K49R, H80S, P81R, V82L, E84P, A87F, T89V and R107K
 CC amino acid substitutions; these residues are conserved in the
 CC human light chain (kappa chain). Host cell Escherichia coli
 CC PHSH5 SANK 70398 harbors plasmid PHSH5 carrying a fusion
 CC fragment of the humanised PDHH type HFE7A light chain and DNA
 CC encoding the region of human immunoglobulin kappa chain, and is
 CC deposited as FERM BP-6274 (claimed). The invention provides
 CC methods for producing humanised antibodies by culturing host
 CC cells. Humanised versions of HFE7A (see AAW83031-37), like native
 CC HFE7A, are capable of inducing apoptosis in abnormal cells
 CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal
 CC cells. The humanised antibodies are used to evaluate, in animal
 CC models, treatments of diseases that involve Fas/Fas ligand
 CC interactions, and also to treat such diseases, including autoimmune
 CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
 CC graft versus host disease, Sjogren syndrome, pernicious anaemia,
 CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
 CC sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
 CC thrombopenia purpura and insulin-dependent diabetes), allergies,
 CC atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
 CC nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
 CC rejection (all claimed).
 XX
 SQ Sequence 238 AA;

Query Match

95.5%; Score 11193; DB 19; Length 238;

Best Local Similarity 95.8%; Pred. No. 2,1e-62;

Matches 228; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 METDTILLWVLLWVGSTGDIIVLTQSPGTLSLSPGERATLSCKASQSVVDYDGSYMMWY 60
 DB 1 metdtillwvllwvgstgeivltqspgtlspsgeratlsckasqsvdydgdsymwyy 60
 QY 61 QOKPGQPPKLLIYAANLESIGIPDRFSGSGCTDFTLTTHPVEEDAAATYYCQSNEDPR 120
 DB 61 gqkpgqpprlliyadnlesigipdrfsgsgtdftltisrlepedfavyycqsgnedpr 120
 QY 121 TFGQGTREIKRTVAAPSVFIFPPSDEOLKSGTASVCLLNNFYPREAKVQWKVNALQS 180
 DB 121 tfgqgtkieikrtvapsvfifppdsedqlksgtasvcllnnfybreakvqwkvdnalqs 180
 QY 181 GNSQSVTEQDSKSTYSLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238
 DB 181 gnsqsvteqdsksyslsstltlskadyekhkyvacevthqglsspvtksfnrgec 238

RESULT 14

AAB14777

ID AAB14777 standard; Protein: 238 AA.

XX AC AAB14777;

XX XX 24-NOV-2000 (first entry)

DE Humanised anti-Fas antibody light chain, SEQ ID NO:107.

KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; humanised antibody; complementarity determining region; CDR;
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
 KW hepatitis; AIDS; graft rejection; light chain.

OS Chimeric - Mus musculus.

OS Chimeric - Homo sapiens.

PN JP2000169393-A.

XX PD 20-JUN-2000.

XX PF 30-SEP-1999; 99JP-0278301.

XX PR 30-SEP-1998; 98JP-0276883.

XX PA (SANY) SANKYO CO LTD.

XX DR WPI: 2000-485645/43.

XX DR N-PSDB; AAA72176.

PT Preventive or treating agent for the diseases caused by an abnormality
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody

PS Claim 20; Page 101; 339pp; Japanese.

XX The invention relates to compositions for the prevention or treatment
 XX or diseases caused by an abnormality in the Fas/Fas ligand system
 XX containing an anti-Fas antibody as the active component. The anti-Fas
 XX antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 XX or a humanised version of HFE7A containing identical CDRs
 XX (complementarity determining regions) to antibody HFE7A. Via its
 XX interaction with Fas, the antibody of the invention acts as a modulator
 XX of apoptosis. The composition of the invention may therefore be used in
 XX the treatment or prevention of conditions such as autoimmune diseases,
 XX allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 XX glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 XX and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
 XX represent the light chains of several humanised HFE7A-derived anti-Fas

CC antibodies.
 XX
 SQ Sequence 238 AA;

Query Match 95.5%; Score 1193; DB 21; Length 238;
 Best Local Similarity 95.8%; Pred. No. 2.1e-62;
 Matches 228; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 METDTILLWLLWVPGSTGDIVLTQSPGTLISLSPGERATLSCSKASQSDYDGDSDYNNWY 60
 Db 1 metdtillwllwvpgstgeivltqspgtlslspgeratlscskasqsdvdygdsymnw 60

QY 61 QOKPQPKLLIYAASNLESGIPDRFSGSGGTDTLTITHPVEEDAATYYCQOSNEDPR 120
 Db 61 qkpgqprrlliyaasnlesgipdrfsgsggtftltisrlepedfavyycqgsnedpr 120

QY 121 TFGQGTREIKRTVAAPSVFIFPPSDQLKSGTASVVCLLNFFPREAKVQWKVDNALQS 180
 Db 121 tfgggtkleikrtvaapsvfifppsdqlksgtasvvcvllnnfypreakvqwkvdnalqs 180

QY 181 GNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238
 Db 181 gnsqesvteqdsksdystlslstltlskadyekhkvyacevthqglsspvtksfnrgec 238

RESULT 15
 AAW90927
 ID AAW90927 standard; Protein; 238 AA.
 XX
 AC AAW90927;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Humanised HFE7A designed light chain protein.
 XX
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX
 OS Synthetic.
 XX
 PN EP990663-A2.
 XX
 PD 05-APR-2000.
 XX
 PF 29-SEP-1999; 99EP-0307711.
 XX
 PR 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX WPI: 2000-258930/23.
 DR N-PSDB; AAA11614.
 XX
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems
 XX
 PS Claim 3; Page 141-142; 263pp; English.
 XX
 CC This invention describes a novel humanized anti-Fas antibody-like

CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A designed light chain which is used in
 CC the method described in the invention.
 XX
 SQ Sequence 238 AA;

Query Match 95.5%; Score 1193; DB 21; Length 238;
 Best Local Similarity 95.8%; Pred. No. 2.1e-62;
 Matches 228; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 METDTILLWLLWVPGSTGDIVLTQSPGTLISLSPGERATLSCSKASQSDYDGDSDYNNWY 60
 Db 1 metdtillwllwvpgstgeivltqspgtlslspgeratlscskasqsdvdygdsymnw 60

QY 61 QOKPQPKLLIYAASNLESGIPDRFSGSGGTDTLTITHPVEEDAATYYCQOSNEDPR 120
 Db 61 qkpgqprrlliyaasnlesgipdrfsgsggtftltisrlepedfavyycqgsnedpr 120

QY 121 TFGQGTREIKRTVAAPSVFIFPPSDQLKSGTASVVCLLNFFPREAKVQWKVDNALQS 180
 Db 121 tfgggtkleikrtvaapsvfifppsdqlksgtasvvcvllnnfypreakvqwkvdnalqs 180

QY 181 GNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238
 Db 181 gnsqesvteqdsksdystlslstltlskadyekhkvyacevthqglsspvtksfnrgec 238

Search completed: April 24, 2002, 15:09:52
 Job time: 95 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 15:10:40 ; Search time 42.08 Seconds
(without alignments)
127.276 Million cell updates/sec

Title: US-09-499-662-54

Perfect score: 1249

Sequence: 1 METDRIILLWLLLVPGSTG.....EVTGGLSPVTKSPNRGEC 238

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1030	82.5	218	5	PCT-US96-13152-2
2	1016	81.3	218	2	US-08-887-352B-13
3	1016	81.3	218	3	US-08-466-151-9
4	1016	81.3	218	4	US-09-109-207C-13
5	1016	81.3	218	4	US-09-296-005-13
6	993	79.5	218	4	US-09-282-505-1
7	993	79.5	218	4	US-09-054-255-1
8	990	79.3	218	2	US-08-887-352B-15
9	990	79.3	218	2	US-08-887-352B-17
10	990	79.3	218	2	US-08-887-352B-19
11	990	79.3	218	2	US-08-887-352B-24
12	990	79.3	218	4	US-09-109-207C-15
13	990	79.3	218	4	US-09-109-207C-17
14	990	79.3	218	4	US-09-109-207C-19
15	990	79.3	218	4	US-09-109-207C-24
16	990	79.3	218	4	US-09-296-005-15
17	990	79.3	218	4	US-09-296-005-17
18	990	79.3	218	4	US-09-296-005-19
19	990	79.3	218	4	US-09-296-005-24
20	980.5	78.5	241	2	US-07-916-098A-56
21	970.5	77.7	239	3	US-08-487-550-6
22	954	76.4	234	4	US-09-049-672A-6
23	938.5	75.1	233	2	US-07-934-373C-25
24	938.5	75.1	233	3	US-08-437-642B-25
25	938.5	75.1	233	5	PCT-US93-07832-25
26	938.5	75.1	235	4	US-09-171-945-97
27	935	74.9	214	2	US-07-934-373C-39

28	935	74.9	214	3	US-08-437-642B-39	Sequence 39, Appl
29	935	74.9	214	5	PCT-US93-07832-39	Sequence 39, Appl
30	931	74.5	236	1	US-08-157-101A-5	Sequence 5, Appl
31	930.5	74.5	235	4	US-09-171-945-99	Sequence 99, Appl
32	930	74.5	214	2	US-07-934-373C-40	Sequence 40, Appl
33	930	74.5	214	2	US-08-788-800-11	Sequence 11, Appl
34	930	74.5	214	3	US-08-437-642B-40	Sequence 40, Appl
35	930	74.5	214	3	US-09-097-309-2	Sequence 2, Appl
36	930	74.5	214	4	US-09-097-171A-2	Sequence 2, Appl
37	930	74.5	214	5	PCT-US93-07832-40	Sequence 40, Appl
38	930	74.5	237	3	US-09-097-309-6	Sequence 6, Appl
39	930	74.5	237	4	US-09-097-171A-10	Sequence 10, Appl
40	930	74.5	237	4	US-09-422-712B-2	Sequence 2, Appl
41	930	74.5	237	4	US-09-607-756-2	Sequence 2, Appl
42	929.5	74.4	235	4	US-09-171-945-52	Sequence 52, Appl
43	927.5	74.3	235	1	US-08-276-852-153	Sequence 153, App
44	927.5	74.3	235	1	US-08-899-575-153	Sequence 153, App
45	927.5	74.3	235	1	US-08-899-575-153	Sequence 153, App

ALIGNMENTS

RESULT 1

PCT-US96-13152-2
; Sequence 2, Application PC/TUS9613152
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich, et al.
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; ADDRESSEE: Attn: Norman D. Hanson
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13152
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: 27-Dec-95
; APPLICATION NUMBER: EP 95 112 895.8
; FILING DATE: 17-Aug-95
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 19-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Norman D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-13152-2

Query Match 82.5%; Score 1030; DB 5; Length 218;
Best Local Similarity 89.9%; Pred. No. 1.8e-76;

Qy 141 IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 200
Db 121 IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
Qy 201 STLTLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 4

US-09-109-207C-13
; Sequence 13, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; PRIOR APPLICATION NUMBER: 1998-06-30
; PRIOR FILING DATE: US 60/051,554
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-13

Query Match 81.3%; Score 1016; DB 4; Length 218;
Best Local Similarity 88.5%; Pred. No. 2.5e-75;
Matches 193; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

Qy 21 DIVLTQSPGTLSSLSPGERATLSCKASQSDVDYDGSYNNWYQKPGQPPKLLIYAASNLES 80
Db 1 DIQLTQSPSSLASVSGDRVTITCRASQSDVDYDGSYNNWYQKPGKAPKLLIYAASYLE 60
Qy 81 GIPDRFSGSGGTDFTLTIHPVEEEDAATYYCQSNEDPRTFGQGTREIKRTVAAPSVF 140
Db 61 GVPDRFSGSGGTDFTLTISSLPQEDFATYYCQSHEDPRTFGQGTREIKRTVAAPSVF 120
Qy 141 IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 200
Db 121 IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
Qy 201 STLTLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 5

US-09-296-005-13
; Sequence 13, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial

; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-296-005-13

Query Match 81.3%; Score 1016; DB 4; Length 218;
Best Local Similarity 88.5%; Pred. No. 2.5e-75;
Matches 193; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

Qy 21 DIVLTQSPGTLSSLSPGERATLSCKASQSDVDYDGSYNNWYQKPGQPPKLLIYAASNLES 80
Db 1 DIQLTQSPSSLASVSGDRVTITCRASQSDVDYDGSYNNWYQKPGKAPKLLIYAASYLE 60
Qy 81 GIPDRFSGSGGTDFTLTIHPVEEEDAATYYCQSNEDPRTFGQGTREIKRTVAAPSVF 140
Db 61 GVPDRFSGSGGTDFTLTISSLPQEDFATYYCQSHEDPRTFGQGTREIKRTVAAPSVF 120
Qy 141 IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 200
Db 121 IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
Qy 201 STLTLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 6

US-09-282-505-1
; Sequence 1, Application US/09282505A
; Patent No. 6194551
; GENERAL INFORMATION:
; APPLICANT: Esohe Ekinaduse Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R1
; CURRENT APPLICATION NUMBER: US/09/282,505A
; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-218
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6194551
US-09-282-505-1

Query Match 79.5%; Score 993; DB 4; Length 218;
Best Local Similarity 86.7%; Pred. No. 1.8e-73;
Matches 189; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

Qy 21 DIVLTQSPGTLSSLSPGERATLSCKASQSDVDYDGSYNNWYQKPGQPPKLLIYAASNLES 80
Db 1 DIQLTQSPSSLASVSGDRVTITCRASQSDVDYDGSYNNWYQKPGKAPKLLIYAASYLE 60
Qy 81 GIPDRFSGSGGTDFTLTIHPVEEEDAATYYCQSNEDPRTFGQGTREIKRTVAAPSVF 140
Db 61 GVPDRFSGSGGTDFTLTISSLPQEDFATYYCQSHEDPRTFGQGTREIKRTVAAPSVF 120
Qy 141 IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 200
Db 121 IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
Qy 201 STLTLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 7

US-09-054-255-1
; Sequence 1, Application US/09054255

```

RESULT      8
US-08-887-352B-15
; Sequence 15, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids

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nb 1 RIQLTQSPSSI:SA SVGDPRVTITCR

Qy 21 DIVLTQSPGTLSPGERATISCKASQSDYDGDSYMWNWYQKPGQPKLLIYAASNLES 80
|| || || || || : || || || || || : || || || || || : || || || || ||
Db 1 DIOLTSPLSLASVSDRVITTCRAKSPVDGEGPSYLNWYQKPGKAPKLLIYAASYLE 60


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; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 15
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-2076-15

```

Query Match	79.3%	Score 990;	DB 4;	Length 218;
Best Local Similarity	86.2%	Pred. No. 3.2e-73;		
Matches 188;	Conservative 15;	Mismatches 15;	Indels 0;	Gaps 0;
QY	21	DIVLTQSPGTLSTLSPGGRATLSCRKASQSDVDGDSYNNWYQOKGQPPKLLIYAASNLNES	80	
		: : : : : : : : : : : : : :		
Db	1	DIQLTSPSSILSASVGDRTVITCRASFPVGDGSDYLNWYQOKGKAPKLLIYAASYLES	60	
QY	81	GIPDRFSGSGSDFTLTITHPVEEDATATYCCQSNEDPRTFGGOTRLKRTVAAPSVF	140	
		: : : : : : : : : : : : :		
Db	61	GVPSRFSGSGSDFTLTITSSLPQDEPATYCCQSHEDPYTFGGCTKVEIKRTVAAPSVF	120	
QY	141	IFPPSDQLKSGTASVYCVLLNFFPRACKQWKVDNALQSNQSQSPYTFEQDSKOSTYSL	200	
		: : : : : : : : : : : : :		
Db	121	IFPPSDQLKSGTASVYCVLLNFFPRACKQWKVDNALQSNQSQSPYTFEQDSKOSTYSL	180	
QY	201	STLTSLKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC	238	
		: : : : : : : : : : : : :		
Db	181	STLTSLKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC	218	

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RESULT 13
US-09-109-207C-17
; Sequence 17, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 17
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-17

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[illegible]

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Db 121 IFPPSDEQLKSGTASVYVCLLNFNYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
Qy 201 STLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 238
    |||||
Db 181 STLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 218
    |||||

RESULT 14
US-09-109-207C-19
; Sequence 19, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improvi
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 19
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain F(ab) sequence derived from MAE11
US-09-109-207C-19

```

Query Match	79.38;	Score 990;	DB 4;	Length 218;
Best Local Similarity	86.2%;	Pred. No. 3.2e-73;		
Matches 188;	Conservative 15;	Mismatches 15;	Indels 0;	Gaps 0;
Qy	21	DIVLTQSPGTLSPGGERATISCKRASQSYVDGDSYNNWYQOKQPQPKLLIIYAASNL	80	
Db	1	DIQLTQSPSSLSASVGDRTITCRASRPVDEGDSYLNWYQOKFGKAPKLLIIYAASYL	60	
Qy	81	GIPDRFGSGSGDTFTLTITHPVEEDAATYYCQOSNEDPRTFFGGOTRLEIKRTVAAPSVF	140	
Db	61	GVPSRFSGSGSGDTFTLTISLQPEDEATYYCQOSHEDPDTFFGGOTKVEIKRTVAAPSVF	120	
Qy	141	IFPSPDQLKSGTASVYVCLLNPNFPRAKQVQWVDNALQSNQSQESVTEQDSKOSTYSL	200	
Db	121	IFPSPDQLKSGTASVYVCLLNPNFPRAKQVQWVDNALQSNQSQESVTEQDSKOSTYSL	180	
Qy	201	STLTSLKADYEKKHYVACEVTHQGLSSPVTKSFNRGEC	238	
Db	181	STLTSLKADYEKKHYVACEVTHQGLSSPVTKSFNRGEC	218	

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RESULT 15
US-09-109-207C-24
; Sequence 24, Application US/09109207C
; Patent No. 6173213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard
; TITLE OF INVENTION: Improved Anti-I
; FILE REFERENCE: P1133R1
; CURRENT APPLICATION NUMBER: US/09/10
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 24
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain Fab

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US-09-109-207C-24

Query Match 79.3%; Score 990; DB 4; Length 218;
Best Local Similarity 86.2%; Pred. No. 3.2e-73;
Matches 188; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

QY	21	DIVLTSPGTLSPGERATLSCKASQSDYDGDSDYNNWYQQRPGQPPKLLIYAASNLES	80
Db	1	DIQLTQSPSSLASVSGDRVTITCRASKPVDGEGSVLNNWYQQRKGRAPKLLIYAASVLES	60
QY	81	GIDPRSGSGGTDFTLTIIHPVEEEDAATYYCOOSNEDPRTFGQGTPLKRTVAAPSVF	140
Db	61	GVPSRFSGSGGTDFTLTIISSLPQPEDFATYYCOOSNEDPRTFGQGTPLKRTVAAPSVF	120
QY	141	IFPPSDEQLKSGTASVVCLLNNFYPREAKYQWKVDNALQSGNSQESVTEQDSKDSSTYSLS	200
Db	121	IFPPSDEQLKSGTASVVCLLNNFYPREAKYQWKVDNALQSGNSQESVTEQDSKDSSTYSLS	180
QY	201	STLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC	238
Db	181	STLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC	218

Search completed: April 24, 2002, 15:10:41
Job time: 144 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 15:11:37 ; Search time 49.97 Seconds
(without alignments)
362.809 Million cell updates/sec

Title: US-09-499-662-54

Perfect score: 1249

Sequence: 1 METDTILLVLLWVPGSTG.....EVTHQGLSSPVTKSFNRGEC 238

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	958.5	76.7	215	2 JE0242	Ig kappa chain NIG
2	919.5	73.6	215	2 JE0244	Ig kappa chain NIG
3	894.5	71.6	215	2 JE0243	Ig kappa chain NIG
4	892.5	71.5	215	2 A23746	Ig kappa chain V-I
5	881	70.5	216	2 JE0241	Ig kappa chain Am3
6	796	63.7	240	2 S06084	Ig kappa chain pre
7	787	63.0	218	2 S68241	Ig kappa chain V r
8	785	62.9	218	2 JC5810	monoclonal antibody
9	770	61.6	210	2 A56169	Ig kappa chain V r
10	728	58.3	220	2 A31790	Ig kappa chain V r
11	714	57.2	234	2 S14237	Ig kappa chain pre
12	710.5	56.9	230	2 S33161	Ig kappa chain - s
13	708.5	56.7	219	2 PC4203	Ig kappa chain (mo
14	705.5	56.5	219	2 S52028	Ig kappa chain - m
15	703.5	56.3	225	2 S37484	Ig kappa chain - m
16	701.5	56.2	219	2 S38865	Ig kappa chain - m
17	700.5	56.1	235	2 S25058	Ig kappa chain - m
18	692.5	55.4	217	2 S42772	Ig kappa chain V r
19	692.5	55.4	219	2 S16112	Ig kappa chain (Ma
20	688	55.1	214	2 S68212	Ig kappa chain pre
21	684	54.8	234	2 S01320	Ig kappa chain pre
22	675.5	54.1	225	2 JL0029	Ig kappa chain pre
23	626	50.1	131	2 PH1226	Ig kappa chain pre
24	622	49.8	178	2 PT0219	Ig kappa chain V-C
25	604.5	48.4	197	2 S29593	Ig kappa chain (WM
26	602.5	48.2	135	2 S52059	JC-kappa protein -
27	602.5	48.2	229	2 A20969	Ig kappa chain pre
28	566.5	45.4	238	2 A49633	Ig lambda-like cha
29	559	44.8	131	1 KVMS6	Ig kappa chain pre

30	548	43.9	106	1 K3HU	Ig kappa chain C r
31	547	43.8	140	2 PNO446	Ig kappa chain pre
32	544	43.6	131	2 S55027	Ig light chain pre
33	541	43.3	144	2 PL0106	Ig kappa chain pre
34	540	43.2	132	1 KVMS32	Ig kappa chain pre
35	528	42.3	111	1 KVMS43	Ig kappa chain V r
36	526	42.1	111	1 KVMS83	Ig kappa chain V r
37	524	42.0	111	1 KVMS08	Ig kappa chain V r
38	523	41.9	112	2 S19971	Ig kappa chain V r
39	521	41.7	111	1 KVMS69	Ig kappa chain V r
40	519.5	41.6	145	2 S20631	Ig kappa chain - h
41	513	41.1	99	2 A37927	Ig kappa chain C r
42	509	40.8	233	2 S29577	Ig light chain - r
43	507	40.6	99	2 S26653	Ig kappa chain C r
44	503.5	40.3	110	1 KVMS10	Ig kappa chain V r
45	503	40.3	111	1 KVMSCL	Ig kappa chain V r

ALIGNMENTS

RESULT 1

JE0242

Ig kappa chain NIG26 precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JE0242

R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinor

submitted to JIPID, November 1998

A:Description: Structure relationship of kappatype light chains with AL amyloidosis

A:Reference number: JE0241

A:Accession: JE0242

A:Molecule type: protein

A:Residues: 1-215 <ALI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 76.7%; Score 958.5; DB 2; Length 215;
Best Local Similarity 85.8%; pred. No. 2e-55;
Matches 187; Conservative 11; Mismatches 17; Indels 3; Gaps 1;

Qy	21	DIVLTQSPGTLSLSPGERATLSCASQSYVDYDGSYNNMYQQKPGQPKLLIYAASNLDS	80
Db	1	EIVLTQSPGTLSLSPGERATLSCASQSV---SNNYLAWYQQKPGQAPSLLIYDASSRAT	57
Qy	81	GIPDRFSGSGGTDFTHIHPVEEDATYYCQSNEDPRFTGQGRLEIKRTVAAPSVF	140
Db	58	GIPDRFSGSGGTDFILTISGLEPDAFYVYQYQYDRPPWTFQGKTKVETVAAPSVF	117
Qy	141	IFPPSDEOLKSGTASVWCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYSLS	200
Db	118	IFPPSDEOLKSGTASVWCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYSLS	177
Qy	201	STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC	238
Db	178	STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC	215

RESULT 2

JE0244

Ig kappa chain NIG2 precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JE0244

R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi,

submitted to JIPID, November 1998

A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL

A:Reference number: JE0243

A:Accession: JE0244

A:Molecule type: protein

A:Residues: 1-215 <ALI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 73.6%; Score 919.5; DB 2; Length 215;
Best Local Similarity 83.18; Pred. No. 6.7e-53;
Matches 182; Conservative 11; Mismatches 21; Indels 5; Gaps 2;

Qy 21 DIVLTQSPGTLSPGERATLSCASQSDYDGDSDYNNWYQKPGQPKLLIYAASNLDES 80
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :
Db 1 EWLVTQSPATLSVSPGERATLSCRASQSV---HSNLAWYQKPGQAPRLLIYRASTRAT 56
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :
Qy 81 GIPDRFSGSGGTDTLTITHPVEEEDAATYYCQSQNE--DPRTFGQGRLEIKRTVAAPSV 139
||| :|||||:|||||:||||| : : ||||| :|||: ||| :
Db 57 GIPARFSGSGGTDTLTITSSQSEDFALYCCQYNTWPPLTFGGGRKVEIKRTVAAPSV 116
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :
Qy 140 FIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSL 199
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :
Db 117 FIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSL 176
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :
Qy 200 SSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 238
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :
Db 177 SSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 215
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :

RESULT 3

JE0243

Ig kappa chain NIG93 precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JE0243

R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T

submitted to JIPID, November 1998

A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy

A:Reference number: JE0243

A:Accession: JE0243

A:Molecule type: protein

A:Residues: 1-215 <ALI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 71.6%; Score 894.5; DB 2; Length 215;
Best Local Similarity 80.8%; Pred. No. 2.8e-51;
Matches 177; Conservative 15; Mismatches 22; Indels 5; Gaps 2;

Qy 21 DIVLTQSPGTLSPGERATLSCASQSDYDGDSDYNNWYQKPGQPKLLIYAASNLDES 80
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSV---ATNVVWYMQKLGQAPRLLIYDASTRAT 56
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :
Qy 81 GIPDRFSGSGGTDTLTITHPVEEEDAATYYCQSQNE--DPRTFGQGRLEIK-RTVAAPSV 139
||| :|||||:|||||:||||| : : ||||| :|||: ||| :
Db 57 GVPARFSGSGGTDTLTITSSQSEDFALYCCQYNTWPPLTFGGGRKVEIKRTVAAPSV 116
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :
Qy 140 FIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSL 199
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :
Db 117 FIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSL 176
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :
Qy 200 SSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 238
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :
Db 177 SSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 215
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :

RESULT 4

A23746

Ig kappa chain V-III (KAU cold agglutinin) - human

C:Species: Homo sapiens (man)

C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000

C:Accession: A23746

R:Leon, J.; Ghiso, J.; Goni, F.; Frangione, B.

J. Biol. Chem. 266, 2836-2842, 1991

A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglob

A:Reference number: A23746; MUID:91131575

A:Accession: A23746

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-215 <LEO>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 71.5%; Score 892.5; DB 2; Length 215;
Best Local Similarity 83.4%; Pred. No. 3.7e-51;
Matches 181; Conservative 9; Mismatches 24; Indels 3; Gaps 1;

Qy 21 DIVLTQSPGTLSPGERATLSCASQSDYDGDSDYNNWYQKPGQPKLLIYAASNLDES 80
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :
Db 1 EIVLTQSPATLSVSPGERATLSCGASQSV---SSNLAWYQKPGQAPRLLIYDASSRAT 57
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :
Qy 81 GIPDRFSGSGGTDTLTITHPVEEEDAATYYCQSQNE--DPRTFGQGRLEIKRTVAAPSV 140
||| :|||||:|||||:||||| : : ||||| :|||: ||| :
Db 58 GIPDRFSGSGGTDTLTITSRLEPEDFAVYGGQYQYSSPLTFGGGRKVEIKRTVAAPSV 117
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :
Qy 141 FIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSL 200
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :
Db 118 FIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSL 177
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :
Qy 201 STLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 237
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :
Db 178 STLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 214
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :

RESULT 5

JE0241

Ig kappa chain Am37 precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JE0241

R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda

submitted to JIPID, November 1998

A:Description: Structure relationship of kappa type light chains with AL amyloidosis:

A:Reference number: JE0241

A:Accession: JE0241

A:Molecule type: protein

A:Residues: 1-216 <ALI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-92/Domain: immunoglobulin homology <IMM>

Query Match 70.5%; Score 881; DB 2; Length 216;
Best Local Similarity 80.3%; Pred. No. 2.1e-50;
Matches 175; Conservative 15; Mismatches 26; Indels 2; Gaps 2;

Qy 21 DIVLTQSPGTLSPGERATLSCASQSDYDGDSDYNNWYQKPGQPKLLIYAASNLDES 80
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :
Db 1 DIVLTQSPDFLAVSLGERATINCKSSQSVLYNSKNFLAWYQKPGQ-PKLLIY-ANVRES 58
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :
Qy 81 GIPDRFSGSGGTDTLTITHPVEEEDAATYYCQSQNE--DPRTFGQGRLEIKRTVAAPSV 140
||| :|||||:|||||:||||| : : ||||| :|||: ||| :
Db 59 GVPDRFSGSGGTDTLTITISNLQAEVLAVYCCQYIYTPYFSGGGRLEIKRTVAAPSV 118
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :
Qy 141 FIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSL 200
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :
Db 119 FIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSL 178
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :
Qy 201 STLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 238
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :
Db 179 STLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 216
:||||| :|||:|||||:||||| : : ||||| :|||: ||| :

RESULT 6

S06084

Ig kappa chain precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000

C:Accession: S06084

QY 81 GIPDRFSGSGTDFTLTIHPVEEEDAAITYCQQSNEDPRTFGQGRLEIKRTVAAPSVF 140

Query Match 61.6%; Score 770; DB 2; Length 210;
Best Local Similarity 69.4%; Pred. No. 3e-43;
Matches 145; Conservative 25; Mismatches 39; Indels

Query Match 61.6%; Score 770; DB 2; Length 210;
Best Local Similarity 69.4%; Pred. No. 3e-43;
Matches 145; Conservative 25; Mismatches 39; Indels

Qy 21 DIVLTQSPGTLSPGGERATLSCASQSVVDGSDSYMMWYQKQPGPKLLIYAASNL 80
Db 1 DIVLTQSPASLTSLGQRATISCRASKSVSSGYSHWYQKQPGPKVLIYASNL 60

Qy 81 GIPDRFSGSGGTDTLTIHPVEEEDATYYCQSNEDPRFTGGTGLRIKRTVAAPSV 140
Db 61 GVPFRFSGSGGTDTLNIHPVEEEDATYYCQHSRELPTFTGGTGLRIKRTVAAPSV 120

Qy 141 IFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSNQSVTEQDSKSTYS 200
Db 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSNQSVTEQDSKSTYS 180

Qy 201 STLTLSKADYKHKYACEVTHQGLSSPV 229
Db 181 STLTLSKADYKHKYACEVTHQGLSSPV 209

RESULT 10
A31790
Ig kappa chain V region (17/9) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: A31790
R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an anti-
A:Reference number: A92686; MUID:89034213
A:Accession: A31790
A:Molecule type: mRNA
A:Residues: 1-220 <SCH>
A:Cross-references: GB:M23626; GB:J04061; NID:G533234; PIDN:AAA39162.1; PID:G533235
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 58.3%; Score 728; DB 2; Length 220;
Best Local Similarity 61.4%; Pred. No. 1.7e-40;
Matches 135; Conservative 33; Mismatches 50; Indels 2; Gaps 1;

Qy 21 DIVLTQSPGTLSPGGERATLSCASQSVVDG--DSYMMWYQKQPGPKLLIYAASNL 78
Db 1 DIVMTQSPSLTVAGEKVTMSCTSSQSLFNSGKQKYLTYQKQPGPKVLIYWASTR 60

Qy 79 ESGIPDRFSGSGGTDTLTIHPVEEEDATYYCQSNEDPRFTGGTGLRIKRTVAAPS 138
Db 61 ESGVDPDRFSGSGGTDTLTISSVQAEGLAVIYQNDYSNPLTFGGGKTLKLRADRAPT 120

Qy 139 VFIPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSNQSVTEQDSKSTYS 198
Db 121 VSIFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSNQSVTEQDSKSTYS 180

Qy 199 LSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 MSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 220

RESULT 11
S14237
Ig kappa chain precursor (15C5) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S14237
R:Vandamme, A.M.; Buleas, F.; Bernar, H.; Nelles, L.; Liinen, R.H.; Collen, D.
Eur. J. Biochem. 192, 767-775, 1990
A:Title: Construction and characterization of a recombinant murine monoclonal antibody d
A:Reference number: S14236; MUID:91006173
A:Accession: S14237
A:Molecule type: mRNA
A:Residues: 1-234 <VAND>
A:Cross-references: EMBL:X56394; NID:G51622; PIDN:CAA39805.1; PID:G51623
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 57.2%; Score 714; DB 2; Length 234;
Best Local Similarity 56.7%; Pred. No. 1.4e-39;
Matches 135; Conservative 35; Mismatches 64; Indels 4; Gaps 1;

Qy 1 METDTILLWVLLWVPGSTGDIVLTQSPGTLSPGGERATLSCASQSVVDGSDSYMMWY 60
Db 1 MRTPAQFGLILLWVPGSTGDIVLTQSPGTLSPGGERATLSCASQSVVDGSDSYMMWY 56

Qy 61 QOKPGQPKLLIYAASNLQSGIPDRFSGSGGTDTLTIHPVEEEDATYYCQSNEDPR 120
Db 57 QOKPGKSPKTLIYKGNRLVAGVPSRFGSGGQDYSLTSSLEYDGVVYCLRYDEFPF 116

Qy 121 TFGGTRLEIKRTVAAPSVFIFFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQ 180
Db 117 TFGGTRLEIKRTVAAPSVFIFFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQ 176

Qy 181 GNSQESVTEQDSKSTYSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 238
Db 177 NGVLNSWTDQDSKSTYSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 234

RESULT 12

S33161

Ig kappa chain - sheep

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000

C:Accession: S33161

R:Foley, R.C.; Beh, K.J.

submitted to the EMBL Data Library, July 1990

A:Description: Isolation and characterisation of sheep kappa light chain cDNA.

A:Reference number: S33161

A:Accession: S33161

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-230 <FOL>

A:Cross-references: EMBL:X54110; NID:G297103; PIDN:CAA38046.1; PID:G1364221

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:143-212/Domain: immunoglobulin homology <IMM>

Query Match 56.9%; Score 710.5; DB 2; Length 230;
Best Local Similarity 58.4%; Pred. No. 2.4e-39;
Matches 136; Conservative 37; Mismatches 55; Indels 5; Gaps 2;

Qy 7 LLWVLLW-VPGSGDIVLTQSPGTLSPGGERATLSCASQSVVDGSDSYMMWYQKQPG 65
Db 2 LLGILLWVLLWVPGSGDIVLTQSPGTLSPGGERATLSCASQSVVDGSDSYMMWYQKQPG 57

Qy 66 QPKLLIYAASNLQSGIPDRFSGSGGTDTLTIHPVEEEDATYYCQSNEDPRFTGG 125
Db 58 QAPKLLIYAATRLTDPVPSRFGSGGTDYTLTISNLEANDTATYVCLQYESTPLAFGG 117

Qy 126 TRLEIKRTVAAPSVFIFFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSNQ 185
Db 118 TNVEIKRSDAQSVFLFKPSEQLTGTGVSVCLVNDYFVKDINVKVQDVTQNSFON 177

Qy 186 SVTEQDSKSTYSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 238
Db 178 SFTDQDSKSTYSSTLTLSSEYQSNINACEVSHKSLTALVKSFNRGEC 230

RESULT 13

PC4203

Ig kappa chain (monoclonal antibody MabA34) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000

C:Accession: PC4203

R:Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.

Gene 173, 257-259, 1996

A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a mAb
A:Reference number: PC4202; MUID:97082978
A:Accession: PC4203
A: Molecule type: mRNA
A:Residues: 1-219 <KWA>
A:Cross-references: GB:U29147; NID:g1594225; PIDN:AAC52821.1; PID:g1594226
C:Comment: This protein is specific for human plasma apolipoprotein A-I of high-density lipoprotein (HDL) and is involved in the regulation of lipid metabolism.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:1-112/Domain: V region #status predicted <VRG>
F:113-219/Domain: C region #status predicted <CRG>

Query Match 56.7%; Score 708.5; DB 2; Length 219;
Best Local Similarity 60.3%; Pred. No. 3e-39;
Matches 132; Conservative 36; Mismatches 50; Indels 1; Gaps 1;
QY 21 DIVLTQSPGTLSPGGERATLSCASQSDY-DGDSYMNWYQKPGQSPKLLIYAASNLE 79
Db 1 DVLMTQTPLSPLVSLGDSQASISCRSSQSIHVTNGNTYLEWYLOKPGQSPKLLIYKVSRRF 60
QY 80 SGIPDRFGSGSGTDFTLTHPVEEEDAATYYCOQSNEDPRTFGQTRLEIKRTVAAPSV 139
Db 61 SGVPDRFGSGSGTDFTLKISRVEADLGYYCFQGSHPRTFGGKLEIKRADAAPTV 120
QY 140 FIPTPSDEQLKSGTASVCLLNFPYKPAKQVKNALQSGNSQESVTEQDSKDYSL 199
Db 121 SIPTPSSEQLTSGGASVVCFLNFPYKQINVKWKIDGSRQNGVLNSWTDQDSKDYSLM 180
QY 200 SSTLTSLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 SSTLTLDKDEYERHNSYTCATHTKTSTPIVKSFNRRNC 219

RESULT 14
S52028
Ig kappa chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
A:Accession: S52028
R:van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schots, A.;
submitted to the EMBL Data Library, August 1994
A:Description: Coordinate expression of antibody subunit genes yields high levels of functional protein.
A:Reference number: S52028
A:Accession: S52028
A:Status: preliminary
A: Molecule type: mRNA
A:Residues: 1-219 <VAN>
A:Cross-references: EMBL:L35138; NID:g522336; PIDN:AAA67525.1; PID:g522337
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 56.5%; Score 705.5; DB 2; Length 219;
Best Local Similarity 60.7%; Pred. No. 4.7e-39;
Matches 133; Conservative 33; Mismatches 52; Indels 1; Gaps 1;
QY 21 DIVLTQSPGTLSPGGERATLSCASQSDY-DGDSYMNWYQKPGQSPKLLIYAASNLE 79
Db 1 DVMTQSPLSPLVSLGDSQASISCRSSQSIHVTNGNTYLEWYLOKPGQSPKLLIYKVSRRF 60
QY 80 SGIPDRFGSGSGTDFTLTHPVEEEDAATYYCOQSNEDPRTFGQTRLEIKRTVAAPSV 139
Db 61 SGVPDRFGSGSGTDFTLKISRVEADLGYYCFQGSHPRTFGGKLEIKRADAAPTV 120
QY 140 FIPTPSDEQLKSGTASVCLLNFPYKPAKQVKNALQSGNSQESVTEQDSKDYSL 199
Db 121 SIPTPSSEQLTSGGASVVCFLNFPYKQINVKWKIDGSRQNGVLNSWTDQDSKDYSLM 180
QY 200 SSTLTSLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 SSTLTLDKDEYERHNSYTCATHTKTSTPIVKSFNRRNC 219

RESULT 15
S37484
Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
A:Accession: S37484
R:Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37484
A:Status: preliminary
A: Molecule type: mRNA
A:Residues: 1-225 <DUC>
A:Cross-references: EMBL:X70424; NID:g406254; PIDN:CAA49869.1; PID:g406255
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 56.3%; Score 703.5; DB 2; Length 225;
Best Local Similarity 60.5%; Pred. No. 6.5e-39;
Matches 138; Conservative 30; Mismatches 55; Indels 5; Gaps 2;
QY 11 LLLWPGSGTGDIVLTQSPGTLSPGGERATLSCASQSDYDGDYMNWYQKPGQSPK 70
Db 3 LLLCVSGAHGSIYMTQTPKFLLSAGDRVTITCKASQSVSND----VAMTQKPGQSPKL 58
QY 71 LIYAASNLSEGIPTDFSGSGGTDFTLTHPVEEEDAATYYCOQSNEDPRTFGQTRLEI 130
Db 59 LIYASRYTGVPDRFTGSGYGTFTTSTVQREDLAVYFCQ-DYSSYTFGGTKLEI 117
QY 131 KRTVAAPSVFIPTPSDEQLKSGTASVCLLNFPYKPAKQVKNALQSGNSQESVTEQ 190
Db 118 KRADAAPTVSIRPTPSSEQLTSGGASVVCFLNFPYKQINVKWKIDGSRQNGVLNSWTDQ 177
QY 191 DSKDSTYSLSSTLTSLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 178 DSKDSTYSMSSTLTLDKDEYERHNSYTCATHTKTSTPIVKSFNRRNC 225

Search completed: April 24, 2002, 15:11:37
Job time: 195 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 15:13:45 ; Search time 29.21 Seconds
(without alignments)
298.741 Million cell updates/sec

Title: US-09-499-662-54

Perfect score: 1249

Sequence: 1 METDITLLWLLWVPGSTG.....EVTHQGLSSPVTKSFNRGEC 238

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 segs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SWISSPROT_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	559	44.8	131	1	KV3I_MOUSE
2	548	43.9	106	1	KAC_HUMAN
3	540	43.2	132	1	KV3F_MOUSE
4	528	42.3	111	1	KV3M_MOUSE
5	526	42.1	111	1	KV3N_MOUSE
6	524	42.0	111	1	KV3O_MOUSE
7	521	41.7	111	1	KV3Q_MOUSE
8	503.5	40.3	110	1	KV3P_MOUSE
9	503	40.3	111	1	KV3L_MOUSE
10	492.5	39.4	129	1	KV3L_HUMAN
11	479.5	38.4	129	1	KV3M_HUMAN
12	465	37.2	111	1	KV3R_MOUSE
13	461	36.9	111	1	KV3H_MOUSE
14	457	36.6	111	1	KV3S_MOUSE
15	454	36.3	111	1	KV3J_MOUSE
16	453	36.3	111	1	KV3K_MOUSE
17	451	36.1	111	1	KV3T_MOUSE
18	448	35.9	128	1	KV3K_HUMAN
19	447.5	35.8	129	1	KV3H_HUMAN
20	443	35.5	134	1	KV4C_HUMAN
21	438	35.1	111	1	KV3U_MOUSE
22	435	34.8	111	1	KV3C_MOUSE
23	434	34.7	112	1	KV3G_MOUSE
24	432	34.6	111	1	KV3A_MOUSE
25	427.5	34.2	133	1	KV4B_HUMAN
26	424.5	34.0	112	1	KV3B_MOUSE
27	423	33.9	111	1	KV3D_MOUSE
28	420.5	33.7	109	1	KV3B_HUMAN
29	420	33.6	108	1	KV3V_MOUSE
30	419.5	33.6	109	1	KV3D_HUMAN
31	419	33.5	129	1	KV1W_HUMAN
32	417.5	33.4	133	1	KV2F_HUMAN
33	416	33.3	115	1	KV3I_HUMAN

RESULT 1

ID	KV3I_MOUSE	STANDARD	PRT	131 AA
AC	P01661			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	IG KAPPA CHAIN V-III REGION MOPC 63 PRECURSOR.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE OF 1-35.			
RX	MEDLINE=78235887; PubMed=98179;			
RA	Burstein Y., Schechter I.;			
RT	"Primary structure of N-terminal extra peptide segments linked to			
RT	the variable and constant regions of immunoglobulin light chain			
RT	precursors: implications on the organization and controlled			
RT	expression of immunoglobulin genes."			
RL	Biochemistry 17:2392-2400(1978).			
RN	[2]			
RP	SEQUENCE OF 21-131			
RX	MEDLINE=73140225; PubMed=4691517;			
RA	McKean D.J., Potter M., Hood L.E.;			
RT	"Mouse immunoglobulin chains. Pattern of sequence variation among			
RT	kappa chains with limited sequence differences."			
RL	Biochemistry 12:760-771(1973).			
RN	[3]			
RP	REVISTONS.			
RX	MEDLINE=79012520; PubMed=99744;			
RA	McKean D.J., Bell M., Potter M.;			
RT	"Mechanisms of antibody diversity: multiple genes encode structurally			
RT	related mouse kappa variable regions."			
RL	Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).			
DR	PIR: A01935; KVM5M6.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003596; Ig_V.			
DR	Pfam: PF00047; Ig_V1.			
DR	SMART: SM00406; IgV: 1.			
KW	Immunoglobulin V region; Signal.			
FT	SIGNAL 1 20			
FT	CHAIN 1 20			
FT	DOMAIN 21 131			
FT	DOMAIN 21 43			
FT	COMPLEMENTARITY-DETERMINING 1.			
FT	DOMAIN 44 58			
FT	DOMAIN 59 73			
FT	DOMAIN 74 80			
FT	DOMAIN 81 112			
FT	DOMAIN 113 121			
FT	DOMAIN 122 131			
FT	DISULFID 43 112			
FT	NON_TER 131 131			
SO	SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;			

Query Match

44.8%; Score 559; DB 1; Length 131;

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Best Local Similarity 79.4%; Pred. No. 8.3e-39;
Matches 104; Conservative 16; Mismatches 11; Indels 0; Gaps 0;

Qy 1 METDTLLVLLWLLVPGSGDTLVLTQSPGTLSPGERATLSCAKSQSDVDYDGSYMNWY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 METDTLLVLLWLLVPGSGTNLVLTQSPASLAVSLGQRTATISCRASESDYSGNSFMHWY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 QOKPGQPKLLIYASNLSESGIDPRFSGSGGTDTFTLHPVEEEDAATYYCQSQNEPDR 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 QOKPGQPKLLIYASNLSESGVPARFSGSGRTDTFTLIDPVEADDAATYYCQONNEDPW 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 TFGGQTRLEIK 131
    ||| |||:||||
Db 121 TFGGQTKLEIK 131
    ||| |||:||||

RESULT 2
KAC_HUMAN
ID KAC_HUMAN STANDARD; PRT; 106 AA.
AC P01834;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE IG KAPPA CHAIN C REGION.
GN IGKC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (MYELOMA PROTEIN EU).
RX MEDLINE=71064023; PubMed=5489770;
RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT acid sequence of the light chain."
RL Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds."
RL Biochemistry 9:3188-3196(1970).
RN [3]
RP SEQUENCE (BENCE-JONES PROTEIN TI).
RX MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT Ti). IV. The complete amino acid sequence and its significance for
RT the mechanism of antibody production."
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=81042304; PubMed=6775818;
RA Hieter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;
RT "Cloned human and mouse kappa immunoglobulin constant and J region
RT genes conserve homology in functional segments."
RL Cell 22:197-207(1980).
RN [5]
RP SEQUENCE (BENCE-JONES PROTEIN ROY).
RX Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA Steinmetz-Kayne M., Suter L., Watanabe S.;
RL (In) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press,
RL New York (1969).
RN [6]
RP SEQUENCE (BENCE-JONES PROTEIN CUM).
RX MEDLINE=68242259; PubMed=5586923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
RT type).";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
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RN [7]
RP SEQUENCE (BENCE-JONES PROTEIN AG).
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges."
RL J. Biol. Chem. 244:3550-3560(1969).
RN [8]
RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains."
RL Science 169:56-59(1970).
CC -1- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
CC MARKER, 45-ALA AND 83-LEU.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J00241; AAA58989.1; -
DR EMBL: V00557; CAA23823.1; -
DR PIR: A02116; K3HU.
DR MIM: 147200; -
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_c1.
DR Pfam: PF00047; Ig_c1.
DR SMART: SM00407; Ig_c1.
DR PROSITE: PS00290; Ig_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 26
FT DISULFID 106
FT VARIANT 83
FT VARIANT 83
FT CONFLICT 14
FT CONFLICT 57
FT CONFLICT 57
SQ SEQUENCE 106 AA; 11609 MW; 51984D1FDD372CE8 CRC64;

Query Match 43.9%; Score 548; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 4.9e-38;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 133 TVAAPSVFIFPPSDQLKSGTASVYVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 192
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 TVAAPSVFIFPPSDQLKSGTASVYVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 193 KDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 KDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
KV3F_MOUSE
ID KV3F_MOUSE STANDARD; PRT; 132 AA.
AC P01658;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION MOPC 321 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-37.
```



```
RX MEDLINE=78235887; PubMed=99179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes.;"
RL Biochemistry 17:2392-2400(1978).
RN [2]
RP SEQUENCE OF 21-132.
RX MEDLINE=73140224; PubMed=4120629;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Partial amino acid sequence of a kappa
RT chain.;"
RL Biochemistry 12:749-759(1973).
CC -!- MISCELLANEOUS: THE PARTIAL SEQUENCE OF THE C REGION OF THIS
CC BENCE-JONES PROTEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT
CC REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY
CC RESIDUES.
DR PIR: A01933; KWS32.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Bence-Jones protein; Signal.
FT SIGNAL 1 20
FT CHAIN 21 132 IG KAPPA CHAIN V-III REGION MOPC 321.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 59 73 FRAMEWORK 2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 81 112 FRAMEWORK 3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 122 131 FRAMEWORK 4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON_TER 132 132
SQ SEQUENCE 132 AA; 14523 MW; 9F3B809BB773FBE9 CRC64;

Query Match 43.2%; Score 540; DB 1; Length 132;
Best Local Similarity 71.2%; Pred. No. 2.9e-37;
Matches 94; Conservative 25; Mismatches 13; Indels 0; Gaps 0;

Qy 1 METDTLLWLLVWPGSTGDIIVTQSPGTLSPGERATLSCKASQSDYDGMNMY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 METDTLLWLLVWPGSTGDIIVTQSPASLAVSLGQRATISCKASQSDYDGMNMY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 QOKPCQPKLLIYAASNLSPGSGSGTDTLTTHPVEEEDAAITYCQSNEDPR 120
   ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ZKPGCPKLLIYASNLZSGIPARFSGSGSTBFTLTIBPVZABDVATYFCZSZB2BFW 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 121 TFGGTRLEIKR 132
   |||||:|||||
Db 121 TFGGTRLEIKR 132
   |||||:|||||

RESULT 4
KV3M_MOUSE STANDARD; PRT; 111 AA.
AC P01655;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7043.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.;"
RL Nature 276:785-790(1978).
DR PIR: B01937; KWS83.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38 FRAMEWORK 1.
FT DOMAIN 39 53 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 54 60 FRAMEWORK 2.
FT DOMAIN 61 92 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 93 101 FRAMEWORK 3.
FT DOMAIN 102 111 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 123 92 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Query Match 42.1%; Score 526; DB 1; Length 111;
Best Local Similarity 88.3%; Pred. No. 3.2e-36;
Matches 98; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
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RL Nature 276:785-790(1978).
DR PIR: A01937; KWS43.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38 FRAMEWORK 1.
FT DOMAIN 39 53 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 54 60 FRAMEWORK 2.
FT DOMAIN 61 92 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 93 101 FRAMEWORK 3.
FT DOMAIN 102 111 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 42.3%; Score 528; DB 1; Length 111;
Best Local Similarity 89.2%; Pred. No. 2.2e-36;
Matches 99; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 21 DIVLTQSPGTLSPGERATLSCKASQSDYDGMNMYQOKPGPKLLIYAASNL 80
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSDYDGMNMYQOKPGPKLLIYAASNL 80
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 81 GIPDRFSGSGSTGDTLTTHPVEEEDAAITYCQSNEDPRTFGQTRLEIK 131
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 GIPARFSGSGSTGDTLTTHPVEEEDAAITYCQSNEDPRTFGSGTRLEIK 111
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
KV3N_MOUSE STANDARD; PRT; 111 AA.
AC P01666;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7183.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.;"
RL Nature 276:785-790(1978).
DR PIR: B01937; KWS83.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Query Match 42.1%; Score 526; DB 1; Length 111;
Best Local Similarity 88.3%; Pred. No. 3.2e-36;
Matches 98; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
```

MDLINE=79073152; PubMed=103003;	
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;	
"Rearrangement of genetic information may produce immunoglobulin	
diversity".	
Nature 276:785-790(1978).	
PIR; E01937; KVM569.	
InterPro: IPR003006; Ig_MHC.	
InterPro: IPR003596; Ig_V.	
Pfam: PF00047; Ig_V1.	
SMART; SM00406; IGV; 1.	
Immunoglobulin V region.	
DOMAIN 1 23	
FT DOMAIN 24 38	
FT DOMAIN 24 38	
FT DOMAIN 39 53	
FT DOMAIN 54 60	
FT DOMAIN 61 92	
FT DOMAIN 93 101	
FT DOMAIN 102 111	
FT DISULFID 23 92	
FT NON_TER 111 111	
FT SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;	
Query Match 41.7%; Score 521; DB 1; Length 111;	
Best Local Similarity 87.4%; Pred. No. 8.1e-36;	
Matches 97; Conservative 8; Mismatches 6; Indels 0;	
21 DIVLTQSPGTLISPERATLSCKASQSYVDYDGSYMMWYQKPGQPKLLIYAASNL	
1 DIVLTQSPASVLSGQRATISCKASQSYVDYDGSYMMWYQKPGQPKVLIFAASNL	
81 GIPDRSGSGGVDFTLTTHPVEEDAAATYCCQSNEDPRTFGQGTGLEIK 131	
61 GIPARFSGSGGVDFTLTINHPVEEDAAATYCCQSNEDPWTFGSGTKLEIK 111	
RESULT 8	
KV3P_MOUSE	
ID KV3P_MOUSE STANDARD; PRT: 110 AA.	
AC P01668;	
DT 21-JUL-1986 (Rel. 01, Created)	
DT 21-JUL-1986 (Rel. 01, Last sequence update)	
DT 15-JUL-1999 (Rel. 38, Last annotation update)	
DE IG KAPPA CHAIN V-REGION PC 7210.	
OS Mus musculus (Mouse).	
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi	
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus	
OX NCBI_TaxID=10090;	
RN [1]	
RP SEQUENCE.	
MDLINE=79073152; PubMed=103003;	
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;	
"Rearrangement of genetic information may produce immunoglobulin	
diversity".	
Nature 276:785-790(1978).	
PIR; D01937; KVM510.	
InterPro: IPR003006; Ig_MHC.	
InterPro: IPR003596; Ig_V.	
Pfam: PF00047; Ig_V1.	
SMART; SM00406; IGV; 1.	
Immunoglobulin V region.	
DOMAIN 1 23	
FT DOMAIN 24 38	
FT DOMAIN 39 53	
FT DOMAIN 54 60	
FT DOMAIN 61 92	
FT DOMAIN 93 100	
FT DOMAIN 101 110	
FT DISULFID 23 92	
FT NON_TER 110 110	
FT SEQUENCE 110 AA; 11950 MW; 69F1A5CE88681249 CRC64;	

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Query Match          40.3%; Score 503.5; DB 1; Length 110;
Best Local Similarity 85.6%; Pred. No. 2.1e-34;
Matches 96; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

Qy 21 DIVLTQSPGTLSPGERATLSCRASQSDYDGSYNNWYQKQKQPPLLIYAASNL 80
    ||||| :||: ||||| :||: ||||| :||: ||||| :||: ||||| :||: |||||
Db 1 DIVLTQSPASLAVSLGQRATISCRASQSLDYDGSYNNWYQKQKQPPLLIYAASNL 60
    ||||| :||: ||||| :||: ||||| :||: ||||| :||: ||||| :||: |||||

Qy 81 GIPRFGSGSGTDFTLTIHPVEEDAATYYCQSNEDPRTFGQTRLEIK 131
    ||||| :||: ||||| :||: ||||| :||: ||||| :||: ||||| :||: |||||
Db 61 GIPARFGSGSGTDFTLTIHPVEEDAATYYCHQS-EDPWTFGSGTKLEIK 110

RESULT 9
KV3L_MOUSE
ID KV3L_MOUSE STANDARD; PRT; 111 AA.
AC P01664;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION CBPC 101.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01936; KVMSC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_v.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 93 101 FRAMEWORK 3.
FT DOMAIN 102 111 COMPLEMENTARITY-DETERMINING 4.
FT DISULFID 23 92 FRAMEWORK 4.
FT NON_TER 111 111 BY SIMILARITY.
SQ SEQUENCE 111 AA; 11964 MW; E2BIAD98AD965962 CRC64;

Query Match          40.3%; Score 503; DB 1; Length 111;
Best Local Similarity 85.6%; Pred. No. 2.3e-34;
Matches 95; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 21 DIVLTQSPGTLSPGERATLSCRASQSDYDGSYNNWYQKQKQPPLLIYAASNL 80
    ||||| :||: ||||| :||: ||||| :||: ||||| :||: ||||| :||: |||||
Db 1 DIVLTQSPASLAVSLGQRATISCRASQSDYDGSYNNWYQKQKQPPLLIYAASNL 60
    ||||| :||: ||||| :||: ||||| :||: ||||| :||: ||||| :||: |||||

Qy 81 GIPRFGSGSGTDFTLTIHPVEEDAATYYCQSNEDPRTFGQTRLEIK 131
    ||||| :||: ||||| :||: ||||| :||: ||||| :||: ||||| :||: |||||
Db 61 GIPARFGSGSGTDFTLTIHPVEEDAATYYCQSNEDPRTFGGTKLEIK 111

RESULT 10
KV3L_HUMAN
ID KV3L_HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION HAH PRECURSOR.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. PubMed=3127527;
RX MEDLINE=88171307; Pubmed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
RT J. Exp. Med. 167:840-852(1988).
RL J. Exp. Med. 167:840-852(1988).
CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
LEUKEMIA.
CC PIR; PL0022; K3HUHA.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_v.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match          39.4%; Score 492.5; DB 1; Length 129;
Best Local Similarity 72.7%; Pred. No. 2e-33;
Matches 96; Conservative 13; Mismatches 20; Indels 3; Gaps 1;

Qy 1 METDTILLWLLLVYPSTGDIVLTQSPGTLSPGERATLSCRASQSDYDGSYNNWY 60
    ||||| :||: ||||| :||: ||||| :||: ||||| :||: ||||| :||: |||||
Db 1 METPQALLFLLLWLPDPTGEIVLTQSPGTLSPGERATLSCRASQSV---SSSLAWY 57
    ||||| :||: ||||| :||: ||||| :||: ||||| :||: ||||| :||: |||||

Qy 61 QOKPQKPPKLIYAASNLFGIPRFGSGSGTDFTLTIHPVEEDAATYYCQSNEDPR 120
    ||||| :||: ||||| :||: ||||| :||: ||||| :||: ||||| :||: |||||
Db 58 QOKPQAPRLLIYGASSRATGIPRFGSGSGTDFTLTIISRLPEPFAVYVYQYGTSPR 117
    ||||| :||: ||||| :||: ||||| :||: ||||| :||: ||||| :||: |||||

Qy 121 TFGQGTREIKR 332
    ||||| :||: ||||| :||: ||||| :||: ||||| :||: ||||| :||: |||||
Db 118 TFGQGTREIKR 129

RESULT 11
KV3M_HUMAN
ID KV3M_HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION HIC PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. PubMed=3127527;
RX MEDLINE=88171307; Pubmed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
RT J. Exp. Med. 167:840-852(1988).
CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M

```

CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
 CC LEUKEMIA.
 DR PIR: PL0021; K3HUH1.
 DR HSSP: P01789; 2MCP.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 1 129
 FT DOMAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 56 70 FRAMEWORK 2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 78 109 FRAMEWORK 3.
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 119 129 JK1 SEGMENT.
 FT DISULFID 43 109 BY SIMILARITY.
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match 38.4%; Score 479.5; DB 1; Length 129;
 Best Local Similarity 71.2%; Pred. No. 2.3e-32;
 Matches 94; Conservative 13; Mismatches 22; Indels 3; Gaps 1;

Qy 1 METDTILLWLLVPGSGTGIVLTQSPGTLSPGERATLSCAKASQSYVDYDGDYMMWY 60
 Db 1 METPAQLFLLLLTDTGEIVLTQSPGTLSPGERATLSCRAVSQV---SSSYLAWY 57
 Qy 61 QOKPGPKLLIYAASNLGSDIPRFGSGSGTDTLTINHPVEEADAATYYCOQSNEDPR 120
 Db 58 QOKPGQAPRLIYGASSRATGIPRFGSGSGTDTLTINSLRLEPDXDFAVYVCOQYGSFPW 117
 Qy 121 TFGQGTREIKR 132
 Db 118 TFGQGTKEIKR 129

RESULT 12
 KV3R_MOUSE STANDARD; PRT; 111 AA.
 AC P01670;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION PC 6684.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity.";
 RL Nature 276:785-790(1978).
 DR PIR: A01938; KVM584.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38 FRAMEWORK 1.
 FT DOMAIN 39 53 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 54 60 FRAMEWORK 2.
 FT DOMAIN 61 92 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 93 101 FRAMEWORK 3.
 FT DOMAIN 102 111 FRAMEWORK 4.
 FT DISULFID 23 92 BY SIMILARITY.

Query Match 36.9%; Score 461; DB 1; Length 111;
 Best Local Similarity 78.4%; Pred. No. 5.9e-31;
 Matches 87; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 12039 MW; 1E46988341858526 CRC64;

Query Match 37.2%; Score 465; DB 1; Length 111;
 Best Local Similarity 79.3%; Pred. No. 2.8e-31;
 Matches 88; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Qy 21 DIVLTQSPGTLSPGERATLSCAKASQSYVDYDGDYMMWYQOKPGPKLLIYAASNLG 80
 Db 1 DIVLTQSPASLAVSGQRATISCRASQSVSTSGYSYMMHWYQOKPGPKLLIYLASNLES 60
 Qy 81 GIPDRFGSGSGTDTLTINHPVEEADAATYYCOQSNEDPRTFGQGTREIKR 131
 Db 61 GVPARFGSGSGTDTLTINHPVEEADAATYYCOHSRELPRTFGGGTKEIKR 111

RESULT 13
 KV3H_MOUSE STANDARD; PRT; 111 AA.
 AC P01660;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION PC 3741/TEPC 111.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE (PC 3741).
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity.";
 RL Nature 276:785-790(1978).
 RN [2]
 RP SEQUENCE (TEPC 111).
 RX MEDLINE=79012520; PubMed=99744;
 RA McKean D.J., Bell M., Potter M.;
 RT "Mechanisms of antibody diversity: multiple genes encode structurally
 RT related mouse kappa variable regions";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
 CC -!- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
 DR PIR: A01934; KVM537.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 39 53 FRAMEWORK 2.
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 61 92 FRAMEWORK 3.
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 102 111 FRAMEWORK 4.
 FT DISULFID 23 92 BY SIMILARITY.
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;

Query Match 36.9%; Score 461; DB 1; Length 111;
 Best Local Similarity 78.4%; Pred. No. 5.9e-31;
 Matches 87; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

Qy 21 DIVLTQSPGTLSPGERATLSCAKASQSYVDYDGDYMMWYQOKPGPKLLIYAASNLG 80
 Db 1 DIVLTQSPASLAVSGQRATISCRASESDSYGNFMMHWYQOKPGPKLLIYRASNLG 60
 Qy 81 GIPDRFGSGSGTDTLTINHPVEEADAATYYCOQSNEDPRTFGQGTREIKR 131
 Db 61 GIPARFGSGSGTDTLTINPVEADVAATYYCOQSNEDPYTFGGGTKEIKR 111

```
RESULT 14
KV3S_MOUSE
ID KV3S_MOUSE STANDARD; PRT; 111 AA.
AC P01671; 1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7175.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
CC -1- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
DR PIR; A01935; KVM56.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;

Query Match 36.3%; Score 454; DB 1; Length 111;
Best Local Similarity 76.6%; Pred. No. 2.2e-30;
Matches 85; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

QY 21 DIVLTQSPGTLSPGERATLSCASQSDYDGSYNNWYQKPGQPPKLLIYAASNL 80
Db 1 NIVLTQSPASLAVSLGQRATISCRASESDVSGSFHMYQKPGQPPKLLIYLASNL 60

QY 81 GIPDRFSGSGGTFTLTITHPVEEEDAATYYCQSNEDPRTFGQGTREIK 131
Db 61 GVPARFSGSGGTFTLTITHPVEEEDAATYYCQSNEDPRTFGGTRLEIK 111
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Search completed: April 24, 2002, 15:13:46
Job time: 323 sec

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Query Match 36.6%; Score 457; DB 1; Length 111;
Best Local Similarity 77.5%; Pred. No. 1.2e-30;
Matches 86; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 21 DIVLTQSPGTLSPGERATLSCASQSDYDGSYNNWYQKPGQPPKLLIYAASNL 80
Db 1 DIVLTQSPASLAVSLGQRATISCRASKSVSTSGYSYHMYQKPGQPPKLLIYLASNL 60

QY 81 GIPDRFSGSGGTFTLTITHPVEEEDAATYYCQSNEDPRTFGQGTREIK 131
Db 61 GVPARFSGSGGTFTLTITHPVEEEDAATYYCQHSRELPLTFGAGTRLEIK 111

RESULT 15
KV3J_MOUSE
ID KV3J_MOUSE STANDARD; PRT; 111 AA.
AC P01662;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION ABPC 22/PC 9245.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (ABPC 22).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
RN [2]
RP SEQUENCE (PC 9245).
```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 15:13:10 ; Search time 86.76 Seconds
(without alignments)
401.254 Million cell updates/sec

Title: US-09-499-662-54
Perfect score: 1249
Sequence: 1 METDTLLVLLVLPVSGTG.....EVTGGLSPVTKSFNRGEC 238

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_17.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mmc.*
 - 8: sp_organelle.*
 - 9: sp_phage.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	745.5	59.7	238	11 Q99M37	Q99M37 mus musculus
2	681	54.5	214	11 Q9RIA5	Q9RIA5 mus musculus
3	426.5	34.1	235	11 Q99M11	Q99M11 mus musculus
4	418.5	33.5	109	4 Q9UL78	Q9UL78 homo sapien
5	402	32.2	103	11 Q9UL80	Q9J180 mus musculus
6	387	31.0	108	4 Q9UL77	Q9UL77 homo sapien
7	385.5	30.9	109	4 Q9UL86	Q9UL86 homo sapien
8	384	30.7	108	4 Q9UL70	Q9UL70 homo sapien
9	381	30.5	108	4 Q9UL79	Q9UL79 homo sapien
10	373	29.9	108	4 Q9UL83	Q9UL83 homo sapien
11	365.5	29.3	107	4 Q9UL81	Q9UL81 homo sapien
12	364.5	29.2	109	4 Q9UL85	Q9UL85 homo sapien
13	351	28.1	114	4 Q9UL80	Q9UL80 homo sapien
14	344.5	27.6	106	5 Q9U410	Q9U410 schistosoma
15	334	26.7	107	11 Q9ERZ9	Q9ERZ9 mus musculus
16	330	26.4	99	11 Q9JL74	Q9J174 mus musculus
17	329	26.3	101	11 Q9UL78	Q9J178 mus musculus
18	328	26.3	97	11 Q9UL76	Q9J176 mus musculus
19	322.5	25.8	104	11 Q9JL82	Q9J182 mus musculus

20	319	25.5	298	11	Q9QYF0	Q9QYF0 mus musculu
21	300	24.0	107	11	Q9JL84	Q9J184 mus musculu
22	293	23.5	109	6	Q9N0W5	Q9N0W5 oryctolagus
23	241	19.3	107	4	Q9UL82	Q9UL82 homo sapien
24	230.5	18.5	107	4	Q9NSD6	Q9NSD6 homo sapien
25	230	18.4	130	4	Q9NP29	Q9NP29 homo sapien
26	225	18.0	130	11	Q9D8W4	Q9D8W4 mus musculu
27	201	16.1	484	11	Q99LA6	Q99LA6 mus musculu
28	198	15.9	267	13	Q90529	Q90529 ginglymosto
29	194.5	15.6	463	11	Q99LC4	Q99LC4 mus musculu
30	194	15.5	473	11	Q9D8L4	Q9D8L4 mus musculu
31	185.5	14.9	479	11	Q99M22	Q99M22 mus musculu
32	180.5	14.5	268	13	Q90524	Q90524 ginglymosto
33	180.5	14.5	509	11	Q08907	Q08907 mus musculu
34	180.5	14.5	509	11	Q9QX57	Q9QX57 mus musculu
35	180.5	14.5	513	11	P97797	P97797 mus musculu
36	177.5	14.2	468	11	Q99L31	Q99L31 mus musculu
37	177.5	14.2	506	6	O46631	O46631 bos taurus
38	174	13.9	105	11	Q99JC1	Q99JC1 mus musculu
39	174	13.9	361	4	Q9H1U5	Q9H1U5 homo sapien
40	172	13.8	473	11	Q99L25	Q99L25 mus musculu
41	171.5	13.7	509	11	Q9WTN4	Q9WTN4 mus musculu
42	171	13.7	252	13	Q90568	Q90568 ginglymosto
43	170	13.6	437	11	Q9RIA4	Q9RIA4 mus musculu
44	169.5	13.6	509	11	P97710	P97710 rattus norv
45	169	13.5	398	4	O00241	O00241 homo sapien

ALIGNMENTS

RESULT 1

Q99M37

ID Q99M37 PRELIMINARY; PRT; 238 AA.

AC Q99M37;

DT 01-JUN-2001 (Tremblrel. 17, Created)

DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)

DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)

DE UNKNOWN (PROTEIN FOR MGC:5947).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=MAMMARY TUMOR;

RA Strausberg R.;

RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC002035; AAH02035.1;

SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match	59.7%	Score 745.5;	DB 11;	Length 238;
Best Local Similarity	59.0%	Pred. No. 2.4e-61;		
Matches 138;	Conservative 39;	Mismatches 56;	Indels 1;	Gaps 1;
Qy	6	ILLVLLVLPVSGTGDI	VTOSPGTSLSPGERATLSCKASQSDYD-DGDSTVMNYQOKP	64
Db	5	VRLVLMFWIPASSDDVVNTQTPLSLPGLGQASISCRSQSIVHSNGNTLEWTLQRP	64	
Qy	65	GQPKLLIYAASNLGSGIDPFRFSGSGSGCTDFTLTTHPVEEADAATYYCQNSNEDPRTFQ	124	
Db	65	GQSPKLLIYKSNRFGVDPDRFSGSGSGCTDFTLTLSRVEAEDLGVYCFQGSHPVTFGS	124	
Qy	125	GTRLEIKTVAAPSVFIPPPDEQLKCTASVVCLLNNFYPREAKVKQVDNALQSGNSQ	184	
Db	125	GTLKLEIKRADAAPIVSIPIPPSEQLTSGGASVVCFLNNFYPRKDNVKKIDGSRQNGVL	184	
Qy	185	ESVTEQDSKDSYSLSSLTLSKADYKHYKVCETHOGLSSPVTKSFNRGEC	238	
Db	185	NSWTDDQSKDSYSLSSLTLSKADYKHYKVCETHOGLSSPVTKSFNRGEC	238	

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RESULT 2
Q9RIA5 PRELIMINARY; PRT; 214 AA.
AC Q9RIA5;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Mista S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF152371; AAD40242.1; -.
DR HSP; P01789; IMCP.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; Ig_v; 1.
DR SMART; SM00410; Ig_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 54.5%; Score 681; DB 11; Length 214;
Best Local Similarity 58.7%; Pred. No. 2e-55;
Matches 128; Conservative 32; Mismatches 54; Indels 4; Gaps 1;

Qy 21 DIVLTQSPGTLSPGERATLSCASQSDVDGDSYMNWYQKPGQPKLLIYAASNL 80
Db 1 DIQLQSPSSMYASIGERVITCKASQDI---NSYLSWFOQKPGKSPKLLIYRANRLVD 56

Qy 81 GIPDRFSGSGGTDFTLTHPVEEEDAATYYCQSNEDPRTFGQGTREIKRTVAAPSVF 140
Db 57 GVPFRSGSGSQDYSLSISSEYEDMGIIYCLQYDEFFTFGSGTKLEIKRADAPTVS 116

Qy 141 IPPPSDEQLKSTASVCLLNFPYREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 200
Db 117 IPPPSSEQLTSGASVCLLNFPYREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 176

Qy 201 SPLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 177 SPLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 3
Q99M11 PRELIMINARY; PRT; 235 AA.
AC Q99M11;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR MCG:6743).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002129; AAH02129.1; -.

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SQ SEQUENCE 235 AA; 25403 MW; 39807BFE6782A3FB CRC64;

Query Match 34.1%; Score 426.5; DB 11; Length 235;
Best Local Similarity 42.6%; Pred. No. 9.1e-32;
Matches 101; Conservative 35; Mismatches 88; Indels 13; Gaps 7;

Qy 7 LLWVLLVPGSTGDIVLTQSPGTLSPGERATLSCASQSDVDGDSYMNWYQKPGQ 66
Db 6 LLVFLHLHTGSCAQLVLTQ--PSSVSTSLGSLAKLPCKA--STGNIGDSYVNWYQYMG 62
Qy 67 PKLLIYAASNLDESIPDRFSGS--GSGTDFTLTHPVEEEDAATYYCQSNEDPRTFGQ 124
Db 63 SPTNMIYGDLLRPSGVSDFSGSIDSSNSAFLTQNVQADDEADYYCQSYSGIRVFGG 122
Qy 125 GTRLEI-KRTVAAPSVFIFPPSDEQLKSGTASVCLLNFPYREAKVQWKVDNALQSGNS 183
Db 123 GTRLEI-KRTVAAPSVFIFPPSDEQLKSGTASVCLLNFPYREAKVQWKVDNALQSGNS 183
Qy 184 QESVTEQDSK--DSYLSSTLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 180 QGVETQSPSKNNKYMASSYLTLTAKAWETHSSSCQVTHGEG--HTVEKSLSRADC 234

RESULT 4
Q9UL78 PRELIMINARY; PRT; 109 AA.
AC Q9UL78;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Vander Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN
DR EMBL; AF035036; AAD56272.1; -.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig_v; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 33.5%; Score 418.5; DB 4; Length 109;
Best Local Similarity 73.2%; Pred. No. 1.9e-31;
Matches 82; Conservative 9; Mismatches 18; Indels 3; Gaps 1;

Qy 21 DIVLTQSPGTLSPGERATLSCASQSDVDGDSYMNWYQKPGQPKLLIYAASNL 80
Db 1 EIVLTQSPGTLSPGERATLSCASQSV---SSSYLAWYQKPGQAPRLIYGASSRAT 57

Qy 81 GIPDRFSGSGGTDFTLTHPVEEEDAATYYCQSNEDPRTFGQGTREIKR 132
Db 58 GIPDRFSGSGGTDFTLTHPVEEEDAATYYCQSNEDPRTFGQGTREIKR 109

RESULT 5
Q9JL80 PRELIMINARY; PRT; 103 AA.
ID Q9JL80

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AC Q9JL80;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Maikiel S.; Liao L.; Cunningham M.W.; Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF206026; AAF69324.1; -.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 103
SQ SEQUENCE 103 AA; 11224 MW; EC87D653DB3AAB21 CRC64;

Query Match 32.2%; Score 402; DB 11; Length 103;
Best Local Similarity 72.3%; Pred. No. 6.1e-30;
Matches 74; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

QY 30 TSLSPGERATLSCKASQSDYDGDSDYNNWYQKPGPPKLLIYAASNLGSDPDRSGS 89
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 2 SLAVSLQRATISCRASEVEYGTSLMNYQKPGPPKLLIYAASNVSGVPARSGS 61

QY 90 GSGTDFTLTHPVEEDAATYVCOQSNEDPRTFGQGTREIKR 131
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 62 GSGTDFSLNHPVEEDDIAMVFCQSRKVPWTGSGGPKLEIK 103

RESULT 6
Q9JL77 PRELIMINARY; PRT; 108 AA.
AC Q9JL77;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF035028; AAD56264.1; -.
DR HSSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 30.9%; Score 385.5; DB 4; Length 109;
Best Local Similarity 68.8%; Pred. No. 2.2e-28;
Matches 77; Conservative 10; Mismatches 22; Indels 3; Gaps 1;

QY 21 DIVLTQSPGTLSPGERATLSCKASQSDYDGDSDYNNWYQKPGPPKLLIYAASNLG 80
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 EIVLTQSPGTLSPGERATLSCKASQSV---SSYLAWYQKPGQAPRLLIYGTSSRAT 57

QY 81 GIPDRFSGSGGTFTLTTHPVEEDAATYVCOQSNEDPRTFGQGTREIKR 132
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 58 GIPDRFSGSGGTFTLTISRLEPEDFAVYVCOQYGSSTFTFGPGTKVDIKR 109

RESULT 8
Q9JL70 PRELIMINARY; PRT; 108 AA.
AC Q9JL70;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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Query Match 31.0%; Score 387; DB 4; Length 108;
Best Local Similarity 65.3%; Pred. No. 1.6e-28;
Matches 73; Conservative 17; Mismatches 18; Indels 4; Gaps 1;

QY 21 DIVLTQSPGTLSPGERATLSCKASQSDYDGDSDYNNWYQKPGPPKLLIYAASNLG 80
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 DIQMTQSPSSLSASVGDRVTITCRASQSI----SSYLNWYQKPGKAPNLIIYAASLSQS 56
NCBI_TaxID=10090;

QY 81 GIPDRFSGSGGTFTLTTHPVEEDAATYVCOQSNEDPRTFGQGTREIKR 132
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 57 GVPDRFSGSGGTFTLTISRLEPEDFAVYVCOQYGSSTFTFGPGTKVDIKR 108
NCBI_TaxID=9606;

RESULT 7
Q9JL86 PRELIMINARY; PRT; 109 AA.
AC Q9JL86;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF035028; AAD56264.1; -.
DR HSSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 30.9%; Score 385.5; DB 4; Length 109;
Best Local Similarity 68.8%; Pred. No. 2.2e-28;
Matches 77; Conservative 10; Mismatches 22; Indels 3; Gaps 1;

QY 21 DIVLTQSPGTLSPGERATLSCKASQSDYDGDSDYNNWYQKPGPPKLLIYAASNLG 80
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 EIVLTQSPGTLSPGERATLSCKASQSV---SSYLAWYQKPGQAPRLLIYGTSSRAT 57

QY 81 GIPDRFSGSGGTFTLTTHPVEEDAATYVCOQSNEDPRTFGQGTREIKR 132
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 58 GIPDRFSGSGGTFTLTISRLEPEDFAVYVCOQYGSSTFTFGPGTKVDIKR 109
NCBI_TaxID=9606;

RESULT 8
Q9JL70 PRELIMINARY; PRT; 108 AA.
AC Q9JL70;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035044; AAD56280.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 30.7%; Score 384; DB 4; Length 108;
Best Local Similarity 64.3%; Pred. No. 3e-28;
Matches 72; Conservative 16; Mismatches 20; Indels 4; Gaps 1;

Qy 21 DIVLTQSPGTLSPGERATLSCASQSDYDGDSDYMMWYQKPGQPKLLIYAASNL 80
Db 1 DLQMTQSPSSLSASVDGRTVITCRASQGI-----SNLAWYQKPGKVPKSLIYAASLTQS 56

Qy 81 GIPDRFSGSGGTFTLTTHPVEEEDAATYYCQSNEDPRTFGQGTLEIKR 132
Db 57 GVPFRSGSGGTFTLTISLQSFEDAVYYCQYSPFPFGQGTKEIKR 108

RESULT 9
Qy 81 GIPDRFSGSGGTFTLTTHPVEEEDAATYYCQSNEDPRTFGQGTLEIKR 132
Db 57 GVPFRSGSGGTFTLTISLQSFEDAVYYCQYSPFPFGQGTKEIKR 108

ID Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035035; AAD56271.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FBAE CRC64;

Query Match 30.5%; Score 381; DB 4; Length 108;
Best Local Similarity 65.2%; Pred. No. 5.7e-28;
Matches 73; Conservative 14; Mismatches 21; Indels 4; Gaps 1;

Qy 21 DIVLTQSPGTLSPGERATLSCASQSDYDGDSDYMMWYQKPGQPKLLIYAASNL 80
Db 1 DIVMTQSPSSLSASTGDRVTISCRMSQGI-----SSYLAWYQKPGKAPPELLIYAASLTQS 56

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Qy 81 GIPDRFSGSGGTFTLTTHPVEEEDAATYYCQSNEDPRTFGQGTLEIKR 132
Db 57 GVPFRSGSGGTFTLTISLQSFEDAVYYCQYSPFPFGQGTKEIKR 108

RESULT 10
Qy 81 GIPDRFSGSGGTFTLTTHPVEEEDAATYYCQSNEDPRTFGQGTLEIKR 132
Db 57 GVPFRSGSGGTFTLTISLQSFEDAVYYCQYSPFPFGQGTKEIKR 108

ID Q9UL83 PRELIMINARY; PRT; 108 AA.
AC Q9UL83;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035031; AAD56267.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 29.9%; Score 373; DB 4; Length 108;
Best Local Similarity 66.1%; Pred. No. 3.2e-27;
Matches 74; Conservative 13; Mismatches 21; Indels 4; Gaps 1;

Qy 21 DIVLTQSPGTLSPGERATLSCASQSDYDGDSDYMMWYQKPGQPKLLIYAASNL 80
Db 1 EIVMTQSPATLSVSPGERATLSCASQSV-----SSNLAWYQKPGQAPRLIYCASTRAT 56

Qy 81 GIPDRFSGSGGTFTLTTHPVEEEDAATYYCQSNEDPRTFGQGTLEIKR 132
Db 57 GIPARFSGSGGTFTLTISLQSFEDAVYYCQHYNNWPFPGTGVKVDIKR 108

RESULT 11
Qy 81 GIPDRFSGSGGTFTLTTHPVEEEDAATYYCQSNEDPRTFGQGTLEIKR 132
Db 57 GIPARFSGSGGTFTLTISLQSFEDAVYYCQHYNNWPFPGTGVKVDIKR 108

ID Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX

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CC DOMAIN.
DR EMBL; AF035033; AAD56269.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match      29.3%; Score 365.5; DB 4; Length 107;
Best Local Similarity 62.5%; Pred. No. 1.5e-26;
Matches 70; Conservative 19; Mismatches 18; Indels 5; Gaps 2;

Qy 21 DIVLTQSPGTLSPGERATLSCASQSDVDGDSYNNWYQKQGPQPKLLIYAASNL 80
Db 1 DIQMTQSPSSUSASVGRVITTCRASQSI----SNLWYQKQKPKAPNLLIYAASLSQ 56

Qy 81 GIPDRFSGSGTDFTLTIHPVEEDAATYYCQSQSDPRFTFGQGTREIKR 132
Db 57 GVPFRSGSGSGTDFTLTISGLQAEATYYCQSQS-YSAITFGGTVDIRR 107

RESULT 12
Q9UL85
ID Q9UL85 PRELIMINARY; PRT; 109 AA.
AC Q9UL85;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035034; AAD56270.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR NON_TER 1
FT NON_TER 114
SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match      28.1%; Score 351; DB 4; Length 114;
Best Local Similarity 58.8%; Pred. No. 3.7e-25;
Matches 67; Conservative 20; Mismatches 25; Indels 2; Gaps 2;

Qy 21 DIVLTQSPGTLSPGERATLSCASQSDYD-DGDSYNNWYQKQGPQPKLLIYAASNL 79
Db 1 DWMTQSPSLPFLTRQPSASISCRSSQSPVSDGNTYLNWFRQGPQPRLLIYKVSND 60

Qy 80 SGIPDRFSGSGTDFTLTIHPVEEDAATYYCQSQSNE-DPRTFGQGTREIKR 132
Db 61 SGVDPFRSGSGSGTDFTLTKISRVEAEDGVYVYCMQGTHTWPPWTFQGTKEIKR 114

RESULT 14
Q9U410
ID Q9U410 PRELIMINARY; PRT; 106 AA.
AC Q9U410;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
OC Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RX Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the light chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF207620; AAF19434.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR NON_TER 1
FT NON_TER 1
```

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CC DOMAIN.
DR EMBL; AF035033; AAD56269.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match      29.3%; Score 365.5; DB 4; Length 107;
Best Local Similarity 62.5%; Pred. No. 1.5e-26;
Matches 70; Conservative 19; Mismatches 18; Indels 5; Gaps 2;

Qy 21 DIVLTQSPGTLSPGERATLSCASQSDVDGDSYNNWYQKQGPQPKLLIYAASNL 80
Db 1 DIQMTQSPSSUSASVGRVITTCRASQSI----SNLWYQKQKPKAPNLLIYAASLSQ 56

Qy 81 GIPDRFSGSGTDFTLTIHPVEEDAATYYCQSQSDPRFTFGQGTREIKR 132
Db 57 GVPFRSGSGSGTDFTLTISGLQAEATYYCQSQS-YSAITFGGTVDIRR 107

RESULT 12
Q9UL85
ID Q9UL85 PRELIMINARY; PRT; 109 AA.
AC Q9UL85;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035034; AAD56270.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR NON_TER 1
FT NON_TER 114
SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match      28.1%; Score 351; DB 4; Length 114;
Best Local Similarity 58.8%; Pred. No. 3.7e-25;
Matches 67; Conservative 20; Mismatches 25; Indels 2; Gaps 2;

Qy 21 DIVLTQSPGTLSPGERATLSCASQSDYD-DGDSYNNWYQKQGPQPKLLIYAASNL 79
Db 1 DWMTQSPSLPFLTRQPSASISCRSSQSPVSDGNTYLNWFRQGPQPRLLIYKVSND 60

Qy 80 SGIPDRFSGSGTDFTLTIHPVEEDAATYYCQSQSNE-DPRTFGQGTREIKR 132
Db 61 SGVDPFRSGSGSGTDFTLTKISRVEAEDGVYVYCMQGTHTWPPWTFQGTKEIKR 114

RESULT 14
Q9U410
ID Q9U410 PRELIMINARY; PRT; 106 AA.
AC Q9U410;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
OC Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RX Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the light chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF207620; AAF19434.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR NON_TER 1
FT NON_TER 1
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Search completed: April 24, 2002, 15:13:10

Region	50..54
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/note= "claim 9"	
69..84	
/label= CDR_H2	
/note= "claim 9"	
118..129	
/label= CDR_H3	
/note= "claim 9"	
AU9859701-A.	
08-OCT-1998.	
30-MAR-1998;	98AU-0059701.
08-OCT-1997;	97JP-0276064.
01-APR-1997;	97JP-0082953.
25-JUN-1997;	97JP-0169088.
(SANY) SANKYO CO LTD.	
Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I; Masahiko O, Nobufusa S, Shin Y, Tohru T; WPI; 1998-543440/47. N-PSDB; AAV70079.	
New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS	
Claim 22; Page 212-213; 292pp; English.	
This is the amino acid sequence of the VD type humanised heavy chain of murine anti-human Fas monoclonal antibody HFE7A. E. coli pgHSL7A62 SANK 73397 harbors plasmid pgHSL7A62 carrying a fusion fragment of the humanised VD type HFE7A heavy chain and DNA encoding human IgG1 constant region (see AAV70079), and is deposited as FERM BP-6074 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AA83031-37), like native HFE7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).	
Sequence	470 AA;
Query Match	100.0%; Score 2515; DB 19; Length 470;
Best Local Similarity	100.0%; Pred. No. 3,9e-143;
Matches 470; Conservative	0; Mismatches 0; Indels 0; Gaps
QY	1 MGWSCIIILFVATATGVHSOVQLVQSAGAEVKKPGASVKYSCKASGYTFTSYMQWKQAP 60
Db	 1 mgwscilflvatatgvhsqvlvqsagaevkkgpgasvkysckasygtfttsymqwkvkap 60
QY	61 GQRLEWMGEIDPDSNTYNQKEFGKATLIVDTVSASTAYMELSSLRSEDTAVYYCARNRD 120
Db	 61 gqrlewmgeidpsdsyntynqqkfkgkatllcvdcasstaymellslrsedtavyycarnrd 120
QY	121 YSNNWYPDMVGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPPEPTVS 180

CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
CC and organ graft rejection. Sequences AAB14775-B14776 and AAB14779
CC represent the heavy chains (or fragments thereof) of various humanised
CC HFE7A-derived anti-Fas antibodies.
XX
SQ Sequence 470 AA;

Query Match 100.0%; Score 2515; DB 21; Length 470;
Best Local Similarity 100.0%; Pred. No. 3.9e-143;
Matches 470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCIIFLVATGATGVSQVQLVQSGAEVKKPGASVKVCKASGYFTFTSWMOWKQAP 60
Db 1 mgwsciiilflvatatgvtghsqvqlvqsgaevkpgasvkckasgyftftswmqwkqap 60
QY 61 GORLEWMEIDPDSYNYNOKFKGKATLTVDTSASTAYMELSLRSEDVAVYCARND 120
Db 61 gqrlwmgelidpsdysnynqkfkgkatltvdtasaymelslrseavtavyccarnd 120
QY 121 YSNWYFDVWGEGLTVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVLDYFPEPTVS 180
Db 121 ysnwnyfdvwegtltvtvssastkgpsvfpplapsskstsagttaalgclvldyfpptvs 180
QY 181 WNSGALTSVGHVTPAVLQSSGLYSLSSVTVVPSSSLGTQYICNVNKHPSNTKVKRVEP 240
Db 181 wnsгалtsvghtfpavilqssglsysslsvtvvpssslgtqyicnvnhkpsntkvdkrvep 240
QY 241 KSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
Db 241 kscdkthtccpapelggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw 300
QY 301 YVDGVEVHNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETIS 360
Db 301 yvdgvevhnaaktpreeqynstyrvvsvltvlhqdwnlgnkeyckvsnkalpapietis 360
QY 361 KAKGQPEQYVLPSPREMTKQVSLTCLVGFYPSDIAVEVSGQENNYKTTTPPV 420
Db 361 kagqpeqyvltppspremtknqvscltclvkgfypsdiavevsgqennytktppv 420
QY 421 LDSGSPFLSKLTVDKSRWQGNVFCVSMHEALHNYTKSLSLSPGK 470
Db 421 ldsdgsfllskltdvksrwqgnvfscvsmhealhnytkslslspgk 470

RESULT 3
AAW90926
ID AAW90926 standard; Protein; 470 AA.

XX AAW90926;
XX
XX 08-AUG-2000 (first entry)
XX Humanised HFE7A designed heavy chain protein.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
XX anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
XX dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
XX nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;
XX hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
XX Hashimoto disease; rheumatoid arthritis; graft versus host disease;
XX Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
XX Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
XX multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
XX insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
XX cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

OS Synthetic.
XX
XX EP990663-A2.
XX
XX 05-APR-2000.
XX
XX

PF 29-SEP-1999; 99EP-0307711.
XX
PR 30-SEP-1998; 98JP-0276881.
XX 30-SEP-1998; 98JP-0276882.
XX
PA (SANY) SANKYO CO.,LTD.
XX
XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX WPI: 2000-258930/23.
DR N-PSDB; AAA11597.
XX
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
XX inflammatory or autoimmune disease, induces apoptosis selectively in
XX cells with abnormal Fas-Fas ligand systems
XX
XX Example reference:15; Page 134-136; 263pp; English.
XX
XX This invention describes a novel humanized anti-Fas antibody-like
XX molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
XX ligand system, by binding to Fas on the cell surface, and prevents
XX apoptosis in cells with a normal system, by inhibiting binding between
XX Fas and its ligand. The products of the invention have anti-inflammatory,
XX anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
XX immunomodulatory, dermatological, immunosuppressive, thyromimetic,
XX antirheumatic, nephrotropic, antinfertility, neuroprotective,
XX antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
XX apoptosis by binding to cell surface Fas or inhibit it by competitive
XX inhibition of ligand binding. (I) are used to treat and/or prevent
XX diseases associated with the Fas/Fas ligand system, especially systemic
XX lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
XX versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
XX anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
XX disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
XX multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
XX dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
XX cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
XX (B, C or D) or alcoholic), and transplant rejection. (I) selectively
XX inhibit apoptosis in normal cells but selectively induce it in abnormal
XX cells. They bind to both human and murine Fas, so can be evaluated in
XX murine disease models. (I) act on the active site of Fas, i.e. they mimic
XX the native ligand, do not induce liver disease, and have reduced risk of
XX inducing a human anti-murine antibody response. This sequence represents
XX a humanised anti-Fas antibody HFE7A designed heavy chain which is used in
XX the method described in the invention.
XX
SQ Sequence 470 AA;

Query Match 100.0%; Score 2515; DB 21; Length 470;
Best Local Similarity 100.0%; Pred. No. 3.9e-143;
Matches 470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCIIFLVATGATGVSQVQLVQSGAEVKKPGASVKVCKASGYFTFTSWMOWKQAP 60
Db 1 mgwsciiilflvatatgvtghsqvqlvqsgaevkpgasvkckasgyftftswmqwkqap 60
QY 61 GORLEWMEIDPDSYNYNOKFKGKATLTVDTSASTAYMELSLRSEDVAVYCARND 120
Db 61 gqrlwmgelidpsdysnynqkfkgkatltvdtasaymelslrseavtavyccarnd 120
QY 121 YSNWYFDVWGEGLTVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVLDYFPEPTVS 180
Db 121 ysnwnyfdvwegtltvtvssastkgpsvfpplapsskstsagttaalgclvldyfpptvs 180
QY 181 WNSGALTSVGHVTPAVLQSSGLYSLSSVTVVPSSSLGTQYICNVNKHPSNTKVKRVEP 240
Db 181 wnsгалtsvghtfpavilqssglsysslsvtvvpssslgtqyicnvnhkpsntkvdkrvep 240
QY 241 KSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
Db 241 kscdkthtccpapelggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw 300

Qy 301 YVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKKVSNAKALPAPIEKTIS 360
 Db 301 yvdgvevhnatkpreeqynstyrvvsvltvlhgdwlngkeyckkvsnkalpapiektis 360
 Qy 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPV 420
 Db 361 kagqgprepgvytlpppreemtknqvslctclvkgyfypsdiavewesngqpennyktppv 420
 Qy 421 LDSGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 470
 Db 421 ldsdgsfflyskltvdksrwqqgnvfscsvmhéalhnnhytqkslspsgk 470

RESULT 4
 AAW83037
 ID AAW83037 standard; Protein; 470 AA.
 AC AAW83037;
 XX DT
 XX 15-MAR-1999 (first entry)
 XX DE Anti-Fas humanised antibody HFE7A heavy chain.
 XX KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy.
 XX OS Homo sapiens.
 OS Synthetic.
 XX PH
 XX FT Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= Sig_peptide
 FT Protein 20..470
 FT /label= Mat_protein
 FT Region 20..140
 FT /label= Variable
 FT Region 141..464
 FT /label= Constant
 FT Region 50..54
 FT /label= CDR_H1
 FT /note= "claim 9"
 FT Region 69..84
 FT /label= CDR_H2
 FT /note= "claim 9"
 FT Region 118..129
 FT /label= CDR_H3
 FT /note= "claim 9"
 XX AU9859701-A.
 XX PN
 XX 08-OCT-1998.
 XX PD
 XX 30-MAR-1998; 98AU-0059701.
 XX PF
 XX 08-OCT-1997; 97JP-0276064.
 XX PR 01-APR-1997; 97JP-0082953.
 XX PR 25-JUN-1997; 97JP-0169088.
 XX XX
 XX (SANY) SANKYO CO LTD.
 XX AKio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 XX Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX WPI; 1998-543440/47.

N-PSDB; AAV70080.

New antibodies and proteins bind conserved epitope of Fas antigen -
 used to evaluate drugs in animal models and to treat Fas-associated
 diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 myocarditis, hepatitis and AIDS

Claim 22; Page 2255227; 292pp; English.

This is the amino acid sequence of the HV type humanised heavy
 chain of murine anti-human Fas monoclonal antibody HFE7A. It
 includes humanising R44G and A76T amino acid substitutions that are
 conserved in the human IgG heavy chain. Host Escherichia coli
 pGHPDHV3 SANK 70298 harbors plasmid pGHPDHV3 carrying a fusion
 fragment of the humanised HV type HFE7A heavy chain and DNA
 encoding human IgG1 constant region (see AAV70080), and is deposited
 as FERM BP-6273 (claimed). The invention provides methods for
 producing humanised antibodies by culturing host cells. Humanised
 versions of HFE7A (see AAW83031-37), like native HFE7A, are capable
 of inducing apoptosis in abnormal cells expressing Fas, and of
 inhibiting Fas-induced apoptosis in normal cells. The humanised
 antibodies are used to evaluate, in animal models, treatments of
 diseases that involve Fas/Fas ligand interactions, and also to
 treat such diseases, including autoimmune disease (e.g. systemic
 lupus erythematosus, Hashimoto's disease, graft versus host disease,
 Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,
 Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,
 autoimmune haemolytic anaemia, sterility, myasthenia gravis,
 multiple scleritis, Basedow's disease, thrombopenia purpura and
 insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
 myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
 anaemia, hepatitis, AIDS and transplant rejection (all claimed).

Sequence 470 AA.

Query Match 99.6%; Score 2504; DB 19; Length 470;
 Best Local Similarity 99.6%; Pred. No. 1.8e-142;
 Matches 468; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MGWSCIILFLVATATGVHSGVQVQSGAEVKKPGASVKVSCKASGYTFTSWMQVKQAP 60
 Db 1 mgwsciilflvatatgvhsqvlvgsgaevkkpgasvkvsckasytfttsywmqvkdap 60
 Qy 61 GORLEWNGEIDPDSYTNYNOKFKGKATLTVDTSASTAYMELSLRSDEDTAVYVCARNRD 120
 Db 61 gqglewngelodpsdytnynokfkkgkatltvdtstastaymelslrsestdavyycarnrd 120
 Qy 121 YSNWYFDVWNGEGLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180
 Db 121 ysnwyfdvwngeglvtvssastkgpsvfpplapskstksggtaalgclvdyfpeptvts 180
 Qy 181 WNSGALTSGVHTFPAIVQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVPE 240
 Db 181 wnsgaltsgvhtfpaviqssglyslssvtvtpssslgtqtyicnvnhkpsntkvdkrvpe 240
 Qy 241 KSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVYDVSHEDPEVKFNW 300
 Db 241 kscdkthtccpcpapellggpsvflfppkpkdtlmisrtpevtcvvydshedpevkfnw 300
 Qy 301 YVDCGEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKKVSNAKALPAPIEKTIS 360
 Db 301 yvdgevhnatkpreeqynstyrvvsvltvlhgdwlngkeyckkvsnkalpapiektis 360
 Qy 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPV 420
 Db 361 kagqgprepgvytlpppreemtknqvslctclvkgyfypsdiavewesngqpennyktppv 420
 Qy 421 LDSGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 470
 Db 421 ldsdgsfflyskltvdksrwqqgnvfscsvmhéalhnnhytqkslspsgk 470

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RESULT 5
AAB14779
ID AAB14779 standard; Protein; 470 AA.
XX
AC AAB14779;
XX
XT 24-NOV-2000 (first entry)
XX
DE Humanised anti-Fas antibody heavy chain, SEQ ID NO:117.
XX
KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-Bp-5828;
KW murine; humanised antibody; complementarily determining region; CDR;
KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
KW hepatitis; AIDS; graft rejection; heavy chain.
XX
OS Chimeric - Mus musculus.
OS Chimeric - Homo sapiens.
XX
PN JP2000169393-A.
XX
PD 20-JUN-2000.
XX
PF 30-SEP-1999; 99JP-0278301.
XX
PR 30-SEP-1998; 98JP-0276883.
XX
PA (SANY ) SANKYO CO LTD.
XX
DR WPI; 2000-485645/43.
DR N-PSDB; AAA72184.
XX
PT Preventive or treating agent for the diseases caused by an abnormality
PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
PT anti-Fas antibody
XX
PS Claim 21; Page 108-109; 139pp; Japanese.
XX
CC The invention relates to compositions for the prevention or treatment
CC or diseases caused by an abnormality in the Fas/Fas ligand system
CC containing an anti-Fas antibody as the active component. The anti-Fas
CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
CC or a humanised version of HFE7A containing identical CDRs
CC (complementarity determining regions) to antibody HFE7A. Via its
CC interaction with Fas, the antibody of the invention acts as a modulator
CC of apoptosis. The compositions of the invention may therefore be used in
CC the treatment or prevention of conditions such as autoimmune diseases,
CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
CC and organ graft rejection. Sequences AAB14775-B14776 and AAB14779
CC represent the heavy chains (or fragments thereof) of various humanised
CC HFE7A-derived anti-Fas antibodies.
XX
SQ Sequence 470 AA;

Query Match 99.68; Score 2504; DB 21; Length 470;
Best Local Similarity 99.68; Pred. No. 1.8e-142;
Matches 468; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGWSCILFLVATATGVRHSOVQLQSGAEVKKPGASVKVSKASGYFTFTSYMMQWVKQAP 60
DB 1 mgwscilflvatatgvrhsqvlqsgaevkpgasvkvsckasgyftftsyymmqqwvkqap 60

QY 61 GQRLWNGEIDPDSYTNYNQKFKGKATLTVDTSTASTAYMELSLRSEDSTAVYYCARNRD 120
DB 61 gqrlwngeldpsdysytnynqkfkgtlvtststastaymelslrsedstavyycarnrd 120

QY 121 YSNWNYFDVWGEGLTVTVSSASTKGPSVFFPLAPSSKTSGGTAAIGCLVDRDYFFPEPTVS 180
DB 121 ysnwnyfdvwwgeglvtvssastkgpsvffplapssktsggtaalgclvdkdyffpeptvs 180

QY 121 ysnwnyfdvwwgeglvtvssastkgpsvffplapssktsggtaalgclvdkdyffpeptvs 180
DB 121 ysnwnyfdvwwgeglvtvssastkgpsvffplapssktsggtaalgclvdkdyffpeptvs 180

QY 181 WNSGALTSGVHTPEAVLQSSCLYSLSSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKRVEP 240
DB 181 wnsгалtsгvhtfpavliqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkrvep 240

QY 241 KSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
DB 241 kscdkthtccppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw 300

QY 301 YVDGVEVHNAKTRPEQYNSTYRVVSVLTVLDHQLMNGKEYCKKVSNNKALPAPIEKTIS 360
DB 301 yvdgvevhnaktreqynstyrvvsvlthdqlmngkeyckkvsnnkalpapiektis 360

QY 361 KAKQCPREPQYATLPPSREEMTKNOVSLTCLVKGFPYSDIAVEHESNQCPENNYKTTTPV 420
DB 361 kkgqcprepqyatlpplsreemtknovsltclvkgfpydsdiaveheshnqcpennyykttppv 420

QY 421 LDSGSPFLYSLKLTVDKSRWQGNVFCVSMHEALHNHYTKSLSLSPGK 470
DB 421 ldsгsрflуslkltvdksrwqgnvfсsmhealhnhytkslslspgk 470

RESULT 6
AAW90929
ID AAW90929 standard; Protein; 470 AA.
XX
AC AAW90929;
XX
DT 08-AUG-2000 (first entry)
XX
DE Humanised HFE7A designed heavy chain protein #2.
XX
KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
KW dermatological; immunosuppressive; thymimetic; antirheumatic; anti-Fas;
KW nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; thrombopenia purpura; allergy;
KW multiple sclerosis; Basedow's disease; arteriosclerosis; myocarditis;
KW insulin dependent diabetes mellitus; glomerulonephritis; hepatitis; transplant rejection.
XX
OS Synthetic.
XX
PN EP990663-A2.
XX
PD 05-APR-2000.
XX
PF 29-SEP-1999; 99EP-0307711.
XX
PR 30-SEP-1998; 98JP-0276881.
XX
PR 30-SEP-1998; 98JP-0276882.
XX
PA (SANY ) SANKYO CO LTD.
XX
PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX
DR WPI; 2000-2589930/23.
DR N-PSDB; AAA11622.
XX
PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems
XX
PS Example reference 22; Page 150-152; 263pp; English.
XX
CC This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,

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CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A designed heavy chain which is used in
 CC the method described in the invention.
 XX
 SQ Sequence 470 AA;

Query Match 99.6%; Score 2504; DB 21; Length 470;
 Best Local Similarity 99.6%; Pred. No. 1.8e-142;
 Matches 468; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MGWSCIIILFLVATATGVHSGVQLVVGSGAEVKKPGASVKVSKCASGYTFTSYVMQVWKQAP 60
 Db 1 mgwsciiilflvatatgvhsqvlvgsgaevkkpgasvkvsckasgytfttsyvmqvwkqap 60
 Qy 61 GORLEWMEIDPSDYTNWYKFKGKATLTVDTASTAYMELSSRSDETAIVYICARNRD 120
 Db 61 ggglewmeidpsdytnynqkfkgaatlvtvdtststaymelsrsrsdetaivyyicarnrd 120
 Qy 121 YSNNNYFDVWGEGTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPPTVTS 180
 Db 121 ysnnyfdvwegegtltvssastkgpsvfplapskstsggtaalgclvdyfppptvts 180
 Qy 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKDKRVEP 240
 Db 181 wnsгалtsgvhtfpavldqssglyslssvstvtpssslgtqtyicnvnhkpsntkdkrvep 240
 Qy 241 KSCDKTHPCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
 Db 241 kscdkthcpcapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw 300
 Qy 301 YVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 360
 Db 301 yvdgvevhnatkpreqynstyrvvsvlvtvlhqdwlngkeyckvsnkalpapiektis 360
 Qy 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGPYPSPDIAVWESNGOPENNYKTTTPV 420
 Db 361 kagqprepqvytlppsreemtqnqslclvkgfypsdiavwesngopennyktttpv 420
 Qy 421 LDSGSEFLYSLKTLVDKSRWQGNVFCVSMHEALHNHYTQKSLSLSPGK 470
 Db 421 ldsdgsfilyslkltvdksrwqgnvfscvsmhealhnhytqkslsislpqk 470

RESULT 7

AAW90933
 ID AAW90933 standard; Protein; 470 AA.

AC AAW90933;

XX 08-AUG-2000 (first entry)

XX Humanised anti-Fas designed heavy chain Heu 1 protein.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;

KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX Synthetic.

OS EP990663-A2.

PN 05-APR-2000.

PD 29-SEP-1999; 99EP-0307711.

PF 30-SEP-1998; 98JP-0276881.

PR 30-SEP-1998; 98JP-0276882.

XX (SANY) SANKYO CO.LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

PI WPI; 2000-259930/23.

DR N-PSDB; AAA11644.73

XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 inflammatory or autoimmune disease, induces apoptosis selectively in
 cells with abnormal Fas-Fas ligand systems

PS Claim 2; Page 169-170; 263pp; English.

XX This invention describes a novel humanized anti-Fas antibody-like

CC molecule (I) that induces apoptosis in cells with an abnormal Fas/Fas

CC ligand system, by binding to Fas on the cell surface, and prevents

CC apoptosis in cells with a normal system, by inhibiting binding between

CC Fas and its ligand. The products of the invention have anti-inflammatory,

CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,

CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,

CC antirheumatic, nephrotropic, cardiant and hepatropic activity. (I) induce

CC apoptosis by binding to cell surface Fas or inhibit it by competitive

CC inhibition of ligand binding. (I) are used to treat and/or prevent

CC diseases associated with the Fas/Fas ligand system, especially systemic

CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft

CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic

CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's

CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,

CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin

CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,

CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral

CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively

CC inhibit apoptosis in normal cells but selectively induce it in abnormal

CC cells. They bind to both human and murine Fas, so can be evaluated in

CC murine disease models. (I) act on the active site of Fas, i.e. they mimic

CC the native ligand, do not induce liver disease, and have reduced risk of

CC inducing a human anti-murine antibody response. This sequence represents

CC a humanised anti-Fas antibody heavy chain construct designated Heu 1

CC which is described in the method of the invention.

XX Sequence 470 AA;

SQ

Query Match 99.4%; Score 2501; DB 21; Length 470;

Best Local Similarity 99.4%; Pred. No. 2.7e-142;

Matches 467; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MGWSCIIILFLVATATGVHSGVQLVVGSGAEVKKPGASVKVSKCASGYTFTSYVMQVWKQAP 60

Db 1 mgwsciiilflvatatgvhsqvlvgsgaevkkpgasvkvsckasgytfttsyvmqvwkqap 60

QY 61 GORLEWMEIDPSDSYTNYNQKFKGKATLTVDTSASTAYMELSSRSEDYAVYYCARNRD 120
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 121 YSNNNYFDWVGEGTLVTYSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYS 180
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 121 YSNNNYFDWVGEGTLVTYSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYS 180
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQYTCNNVNHKPSNTKVDKRVPEP 240
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 241 KSCDKHTCTPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 301 YVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 361 KAKGQPREPQVYTTLPSSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPV 420
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 421 LDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK 470
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 RESULT 8
 AAW90934 standard; Protein: 470 AA.
 XX AAW90934;
 XX 08-AUG-2000 (first entry)
 XX Humanised anti-Fas designed heavy chain Heu 2 protein.
 KW Fas; antibody: human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiatherosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 OS Synthetic.
 XX EP990663-A2.
 XX 05-APR-2000.
 XX 29-SEP-1999; 99EP-0307711.
 XX 30-SEP-1998; 98JP-0276881.
 XX 30-SEP-1998; 98JP-0276882.
 XX (SANY) SANKYO CO LTD.
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 DR WPI; 2000-258930/23.
 DR N-PSDB; AAA11645.
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems

XX Claim 2 : Page 174-176; 263pp; English.

XX This invention describes a novel humanized anti-Fas antibody-like
 XX molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody heavy chain construct designated Heu 2
 XX which is described in the method of the invention.

XX Sequence 470 AA;

Query Match 99.4%; Score 2499; DB 21; Length 470;
 Best Local Similarity 99.1%; Pred. No. 3.5e-142;
 Matches 466; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGWSCIIILFLVATATGVHSQVOLVQSGAEVKKPGASVKVSKASGYTFTSYMQWVKQAP 60
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 61 GORLEWMEIDPSDSYTNYNQKFKGKATLTVDTSASTAYMELSSRSEDYAVYYCARNRD 120
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 121 YSNNNYFDWVGEGTLVTYSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYS 180
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQYTCNNVNHKPSNTKVDKRVPEP 240
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 241 KSCDKHTCTPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 301 YVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 361 KAKGQPREPQVYTTLPSSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPV 420
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 421 LDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK 470
 DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 9
 AAW90935

ID AAW90935 standard; Protein; 470 AA.
 XX AAW90935;
 AC
 DT 08-AUG-2000 (first entry)
 XX
 DE Humanised anti-Fas designed heavy chain Heu 3 protein.
 XX
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antifertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX
 OS Synthetic.
 XX
 PN EP990663-A2.
 XX
 XX 05-APR-2000.
 PD
 XX 29-SEP-1999; 99EP-0307711.
 PF
 XX 30-SEP-1998; 98JP-0276881.
 PR
 PR 30-SEP-1998; 98JP-0276882.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 PI
 XX WPI; 2000-258930/23.
 DR N-PSDB; AA11646.
 XX
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems
 XX
 PS Claim 2; Page 180-182; 263pp; English.
 XX
 CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antifertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody heavy chain construct designated Heu 3
 CC which is described in the method of the invention.
 XX
 SQ Sequence 470 AA;

Query Match 99.3%; Score 2498; DB 21; Length 470;
 Best Local Similarity 99.1%; Pred. No. 4e-142; 2; Indels 0; Gaps 0;
 Matches 466; Conservative 2; Mismatches 2;
 QY 1 MGWSCIIILFVATATGVSQVLVQSGAEVKKPGASVKVSCKASGYTFTSYNMQWYKQAP 60
 DB 1 mgwsciiilfvatatgvsqvlvqsgaevkkpgasvkvsckasgytftsynmqwyrqap 60
 QY 61 GORLEWVGIDSDSYNTNTNQKFKKATLTVDTSATAYMELSSLSRSEDATVAYYCARNRD 120
 DB 61 goglewmgeldpsdsyntntnqkfkgkatltvdtststaymelsslsrse dtavyyca rnr d 120
 QY 121 YNNNYFDVWVGSGTLVTVSSASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180
 DB 121 ynnnyfdv wvgsgtlvtvssastkgpsvfp lapsskstsggtaalgclv kdyfpep tvts 180
 QY 181 WNSGALTSGVHFFPAVLQSSGLYSLSVVTVPSSSISLTQTYICNVNHNKPSNTKVKDRVEP 240
 DB 181 wnsгалtsгvhtfpav lqssg lylsvsvtvps ssslgtqtyicnv nhkpsntkvd rvep 240
 QY 241 KSCDKTHCTCPCPAPPELLGGPSVFLPPTPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
 DB 241 kscdkthctcp cpape llgpsvflpppkdtl misrtpevtcvvvdvsh edpevkfnw 300
 QY 301 YVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 360
 DB 301 yvdgvevhna ktpr eeqynstyrvvsvltvl hqdwlngkeyckvsnkalpapi ektis 360
 QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGSNGPENNKPTTPV 420
 DB 361 kagqprepvytlpps reemtknqvs lclvkgfypsdiavewesngsngpe nnkpttpv 420
 QY 421 LDSGGSFFLYSKLTVDKSRWQQGNVFCSMVHEALHNHYTQKSLSLSPGK 470
 DB 421 ldsdgsfflysk ltyvdksrwqgnvfscsmvheal hnytkls lslspgk 470
 RESULT 10
 AAW90936
 ID AAW90936 standard; Protein; 470 AA.
 XX
 AC AAW90936;
 XX
 DT 08-AUG-2000 (first entry)
 DE
 DE Humanised HFETA designed heavy chain HHH type protein.
 XX
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antifertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX
 OS Synthetic.
 XX
 PN EP990663-A2.
 XX
 XX 05-APR-2000.
 PD
 XX 29-SEP-1999; 99EP-0307711.
 PF
 XX 30-SEP-1998; 98JP-0276881.
 PR
 PR 30-SEP-1998; 98JP-0276882.
 XX
 PA (SANY) SANKYO CO LTD.
 XX

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX WPI; 2000-258930/23.
DR N-PSDB; AAA11655.
XX
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems
XX
XX Claim 2; Page 188-189; 263pp; English.
XX
XX This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thymomimetic,
CC antirheumatic, nephroprotective, antifertility, neuroprotective,
CC antiarteriosclerotic, cardiact and hepatotropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a humanised anti-Fas antibody HFE7A heavy chain construct HHH type
XX which is described in the method of the invention.
XX Sequence 470 AA;

Query Match 98.8%; Score 2485; DB 21; Length 470;
Best Local Similarity 98.5%; Pred. No. 2.4e-141;
Matches 463; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 MGWSCIIILFLVATATGVISQVQLVSGAEVKKPGASVKSCASGYTFTSYMWNQVKAP 60
DB 1 mgwsciiilflvatatgvhsqqlvsgaevkpgasvkscasgytftsywmqvwqap 60
QY 61 GQLEWMEIGDPSDSTYNNQKFKATLTVDTSASTAYMELSLRSEDYAVYYCARND 120
DB 61 99glwemgeidsbstynqkfkvrvtidtskstaymelslrsestavyycarnrd 120
QY 121 YSNNNYFDVWEGTLTVSSASTKGSVFPLAPSSKSTSGGPAALGCLVADYFPEPVTVS 180
DB 121 ysnnyfvdwegtltvssastkgsvfplapskstsggtaalgclvdkyfppeptvs 180
QY 181 WNSGALTSVGHVFPFAVLSSGLYSLSSVTVPPSSSLGTQTYTCNVNHNKPSNTKVDKRVEP 240
DB 181 wnsгалtsvghvfpavlssgylslyssvtpvpsalgtqtyicnvhnkpsntkvdkrvpe 240
QY 241 KSCDKTHPCPCAPPELLGGPSVFLFPPKPKDTLMISPTPEVTCVVVDVSHEDPEVKFNW 300
DB 241 kscdkthcpcapellggpsvflfppkpkdtlmisptpevtcvvvdvshedpevkfnw 300
QY 301 YVDGEVHNAKTKPREQYNTSTYRVSVLTFLHQDLNGKEYCKVKSNKALPAPTEKRTIS 360
DB 301 yvdgevhnaktkpreeqyntstyrsvsvltvlhqdwlngkeyckvkksnkalpapektis 360
QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEVNESGQPPENNYKTTTPV 420
DB 361 kakgqprepqvytlppsreemtknqvsltclvkgyfypsdiavevesngqpennyykttppv 420

DB 361 kakgqprepqvytlppsreemtknqvsltclvkgyfypsdiavevesngqpennyykttppv 420
QY 421 LQSDGSFFLYSKLTVDKSRWQQGNVPSQSVMHREALNHYTKQSLSLSPGK 470
DB 421 ldsdgsfflyskltvdksrwqgnvpsqsvmhrealnhytqkslsispgk 470
RESULT 11
AAW48650
ID AAW48650 standard; Protein; 652 AA.
XX
XX AAW48650;
AC
XX
XX 04-AUG-1998 (first entry)
DE Heavy chain of hmAb425 fused to TNF alpha.
KW Antibody-cytokine fusion protein; triclstronic vector; chimeric;
KW TNF alpha; IL-2; TRES; internal ribosome entry site.
XX Synthetic.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FT Region 1..494
FT /note= "Heavy chain of human mAb 425"
FT Region 495..652
FT /note= "TNF alpha"
XX WO9811241-A1.
XX 19-MAR-1998.
XX 02-SEP-1997; 97WO-EP04765.
XX 30-SEP-1996; 96EP-0115635.
XX 16-SEP-1996; 96EP-0114820.
XX (MERE) MERCK PATENT GMBH.
XX
XX Bruemmer W, Burge C, Dunker R, Hauser H, Mielke C;
PI Rieke E, Von Hoegen I, Weige T;
XX
DR WPI; 1998-207400/18.
XX N-PSDB; AAV18096.
XX
PT Oligo:cistronic expression vector - useful for production of, e.g.
XX MAB425/TNF- α or MAB425/IL-2 antibody fusion protein
XX Disclosure; Fig 15; 89pp; English.
XX
CC The present sequence represents a fusion protein comprising of TNF
CC alpha fused to the C-terminus of the heavy chain of the human
CC monoclonal antibody 425 (hmAb425). The hmAb425 has specificity for
CC the human EGF receptor. The invention claims for a new PMCLDRAP
CC triclstronic vector (AAV18096) for the expression of an
CC antibody-cytokine fusion protein, hmAb425-TNF alpha. The TNF alpha
CC sequence can be substituted by the IL-2 sequence. The vector also
CC contains a strong promoter/enhancer unit, a selection marker gene and at
CC least two poliovirus derived internal ribosomal entry site (IRES)
CC sequences. The vector can be expressed in mammalian host cells for the
CC production of heteromeric fusion proteins. This expression system is
CC claimed to produce the heteromeric proteins in high yields.
XX Sequence 652 AA;

Query Match 91.0%; Score 2288; DB 19; Length 652;
Best Local Similarity 87.5%; Pred. No. 2.1e-129;
Matches 433; Conservative 17; Mismatches 19; Indels 26; Gaps 3;
QY 1 MGWSCIIILFLVATATGVHSQVQLVSGAEVKKPGASVKSCASGYTFTSYMWNQVKAP 60
DB 1 mgwsciiilflvatatgvhsqvlvsgaevkpgasvkscasgytftsywmqvwkqap 60

Db 1 mdwtvrvfcllavagahsqqlvgsgaevkpgasvkscasgytftshwmhwrqap 60
QY 61 GORLEWMEGIDPSDSTNYNQKFKGKATLTVDTSASTAYMELSSLRSEDATVYYCARNRD 120
Db 61 ggglewifegfnggrtnynefkfkatmctvdstntaymelsslrsestavyica-srd 119
QY 121 YS-NMNYFDVWGEGTLVTVSS-----ASTKGPVSFFPLAPSS 155
Db 120 ydydgrfydwgggtlvtvssgewilcawaqlcptprshgttslaastkpgsvfplapss 179
QY 156 KTSGGTAALGLVXDYFPPEPTVTVSNWNGALTSVHTFPFPAVLQSSGLXLSLSSVTVVPSS 215
Db 180 katsgtaalgclvkdypfpvptvswngaltsgvhtfpavlgsglyslssvwtvpss 239
QY 216 LGTQYICNVNHNKPSNTKVKRVEPKSCDKTHTCCPAPPELLGGPSVFLFPKPKDTLM 275
Db 240 lgcqcyicnvnhnkpsntkvdkvepkscdkthtccpapelggpsvflfpkpkdtlm 299
QY 276 ISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNNAKTKPREEQYNSTYRVSVLTVHLQD 335
Db 300 isrtpevtcvvdvshedpevkfnmyvdgvevhnaktkpreeqynstyrsvsvltvlhqd 359
QY 336 WINGKEYCKVSNKALPAPIETISKAKGQPREPQVYITLPPSRREEMTKNQVSLTCLVKGF 395
Db 360 wingkeyckvsnkalpapietiskakgqprepgvvtlppsrdeltnknqslvtclvkqf 419
QY 396 YPSDIAVESNGCPENNYKTTTPPVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEAL 455
Db 420 ypsdlavesngcpennykttppvldsgdsfflyskltvdkswggnvfscsvmheal 479
QY 456 HNHYTQKLSLSPGK 470
Db 480 hnhytqkslspsgk 494

RESULT 12
AAB72228
ID AAB72228 standard; Protein; 465 AA.
XX
AC AAB72228;
XX
DT 10-MAY-2001 (first entry)
XX
DE Humanised 323/A3 (IgG1) antibody heavy chain amino acid sequence.
XX
KW Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis;
KW Chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;
KW heavy chain.
XX
OS Mus sp.
OS Homo sapiens.
XX
PN WO200107082-A1.
XX
PD 01-FEB-2001.
XX
PF 23-JUL-1999; 99WO-EP05271.
XX
PR 23-JUL-1999; 99WO-EP05271.
XX
PA (GLAX) GLAXO GROUP LTD.
PI Knick VC, Stimmel JB, Thurmond LM;
PI
XX WPI: 2001-182729/18.
DR N-PSDB; AAF63374.
XX
PT Combination for treating cancer (e.g. breast, gastric or prostate
PT cancers), or in the manufacture of a medicament for anti-cancer
PT therapy, comprises an anti-Ep-cyclic adenosine monophosphate antibody
PT with a chemotherapeutic agent -
XX
PS Disclosure: Fig 16; 103pp; English.

XX This invention relates to a combination of an anti-Ep-CAM (cyclic
CC adenosine monophosphate) antibody with a chemotherapeutic agent, that is
CC capable of arresting Ep-CAM antigen expressing cells in the synthesis (S)
CC phase or the second growth phase (M) of cell enlargement (G2)/DNA
CC replication. The antibody exhibits cytostatic activity and is useful in
CC the manufacture of a medicament for use in anti-cancer therapy,
CC characterised in that a chemotherapeutic agent, which is capable of
CC arresting Ep-CAM antigen expressing cells in S or in G2/M, is
CC co-administered to a patient with an anti-Ep-CAM antibody. The
CC combination is useful for treating cancer, particularly colorectal
CC cancer, breast cancer, gastric cancer, prostate cancer or non-small-cell
CC lung cancer. The present sequence represents the heavy chain of
CC anti-Ep-CAM antibody known as humanised 323/A3 (IgG1) which can be used
CC in the combination of the invention.
XX
SQ Sequence 465 AA;

Query Match 90.8%; Score 2283.5; DB 22; Length 465;
Best Local Similarity 91.7%; Pred. No. 2.8e-129;
Matches 431; Conservative 14; Mismatches 20; Indels 5; Gaps 2;

QY 1 MGWSCIILFLVATATGVSQVOLVSGAEVKKPGASVKVSKASGYTFTSYNMQWYKQAP 60
Db 1 mgwscililflvatatgvhsqvlvgsgpevkkpgasvkscasgytftnygmnnwvrqap 60
QY 61 GORLEWMEGIDPSDSTNYNQKFKGKATLTVDTSASTAYMELSSLRSEDATVYYCARNRD 120
Db 61 ggglewifegfnggrtnynefkfkatmctvdstntaymelsslrsestavyica-srd 119
QY 121 YS-NMNYFDVWGEGTLVTVSSASTKGPVSFPLAPSSKTSGGTAALGLVXDYFPPEPTV 180
Db 120 ydydgrfydwgggtlvtvssgewilcawaqlcptprshgttslaastkpgsvfplapss 175
QY 156 KTSGGTAALGLVXDYFPPEPTVTVSNWNGALTSVHTFPFPAVLQSSGLXLSLSSVTVVPSS 215
Db 180 katsgtaalgclvkdypfpvptvswngaltsgvhtfpavlgsglyslssvwtvpss 239
QY 216 LGTQYICNVNHNKPSNTKVKRVEPKSCDKTHTCCPAPPELLGGPSVFLFPKPKDTLM 275
Db 240 lgcqcyicnvnhnkpsntkvdkvepkscdkthtccpapelggpsvflfpkpkdtlm 299
QY 276 ISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNNAKTKPREEQYNSTYRVSVLTVHLQD 335
Db 300 isrtpevtcvvdvshedpevkfnmyvdgvevhnaktkpreeqynstyrsvsvltvlhqd 359
QY 336 WINGKEYCKVSNKALPAPIETISKAKGQPREPQVYITLPPSRREEMTKNQVSLTCLVKGF 395
Db 360 wingkeyckvsnkalpapietiskakgqprepgvvtlppsrdeltnknqslvtclvkqf 419
QY 396 YPSDIAVESNGCPENNYKTTTPPVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEAL 455
Db 420 ypsdlavesngcpennykttppvldsgdsfflyskltvdkswggnvfscsvmheal 479
QY 456 HNHYTQKLSLSPGK 470
Db 480 hnhytqkslspsgk 494

RESULT 13
AAB08026
ID AAB08026 standard; Protein; 470 AA.
XX
AC AAB08026;
XX
DT 14-NOV-2000 (first entry)
XX
DE A dimeric anti-CD20 heavy chain polypeptide.
XX
KW Anti-CD20 antibody; dimeric immunoglobulin; immunoglobulin; IgG;
KW complement system; Fc gamma receptor; cytotoxic effector cell;
KW host immune cell; programmed cell death; allergic disorder; cancer;
KW autoimmune disease; allergic asthma; atopic dermatitis; Crohn's disease;
KW allergic bronchopulmonary aspergillosis; allergic rhinitis;
KW Graves's disease; food allergy; allergic contact dermatitis; cancer;
KW B-cell lymphoma; rheumatoid arthritis; ulcerative colitis; psoriasis;

CC cancer, breast cancer, gastric cancer, prostate cancer or non-small-cell
 CC lung cancer. The present sequence represents the heavy chain of
 CC anti-Bp-CAM antibody known as humanised 323/A3 (IgG1) which can be
 CC used in the combination of the invention.
 XX
 SQ Sequence 464 AA;

Query Match 90.6%; Score 2278.5; DB 22; Length 464;
 Best Local Similarity 91.7%; Pred. No. 5.5e-129;
 Matches 430; Conservative 14; Mismatches 20; Indels 5; Gaps 2;

Qy 1 MGWSCIIILFLVATATGVHSQVQLVSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAP 60
 Db 1 mgwsciiilflvatatgvhsqvlvsgaevkpgasvksckasgytftsygmnwvrqap 60
 Qy 61 GORLEWMEIDPSDSTYNYNQKFKGKATLTVDTSASTAYMELSLRSEDATVYYCARNRD 120
 Db 61 g99lewmgwintygeptygedfkgfafsidsastaymelslrseidatavycar--- 117
 Qy 121 YSNNMWYFDVWGEGLVTVSSASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPTVTS 180
 Db 118 fgn--yvdywgsgslvtvssastkgpsvfplapskstsggtaalgclvkdyfpeptvts 175
 Qy 181 WNSGALTSVHTFPFAVLQSSGLYSLSSVTVTPSSSLGTQTYICNNHKNPSNTKVDKRVPEP 240
 Db 176 wnsгалtsгvhtfpavliqssglyslssvttvpssslgtqtyicnnhkpntkvdkkvpep 235
 Qy 241 KSCDKHTCCPPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300
 Db 236 kscdkhtccppcpapellggpsvflppkpkdtlmisrtpevtcvvdvshedpevkfnw 295
 Qy 301 YVDGVEVHNNAKTPREEQYNSTYRVWSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTIS 360
 Db 296 yvdgvevhnaktpreeqynstyrvwsvltvlhqdwlngkeyckvsnkalpapiektis 355
 Qy 361 KAKGQPREPQVYITPPPREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 420
 Db 356 kagqprepqvtyitpppreemtknqvsltcvkgyfypsdiavewesngqpennykttppv 415
 Qy 421 LDSGSEFLYSLKLVDRSRWQGVNFVSCVMHEALHNHYTKQSLSLSPG 469
 Db 416 ldsqseflyslkltvdksrwqgvnfvscvmhealhnhytqkslsispq 464

RESULT 15
 AAE03755
 ID AAE03755 standard; Protein; 466 AA.

AC AAE03755;

XX 07-AUG-2001 (first entry)

XX Chimeric 2403 IgG antibody heavy chain (5F2.4H4.1E3).

XX Murine; prostate stem cell antigen; PSCA; cytostatic; gene therapy;
 KW glycoprotein; cancer; prostate; bladder; lung; tumour; Ab; antibody;
 KW human; immunoglobulin G; IgG; heavy chain region.

XX Chimeric - Mus musculus.

OS Chimeric - Homo sapiens.

XX Key Location/Qualifiers

FF Peptide 1..19

FT /label= Signal_peptide

FT Protein 20..466

FT /label= Mature_IgG_antibody_heavy_chain

FT Region 1..141

FT /note= "Derived from mouse heavy chain variable

FT region (VH)"

FT 142..466

FT /note= "Derived from human IgG heavy chain constant

FT region"

FT

XX WO200140309-A2.
 PN 07-JUN-2001.
 PD

XX 27-OCT-2000; 2000WO-US29603.

XX 29-OCT-1999; 99US-0162558.

XX 16-FEB-2000; 2000US-0182872.

XX (GETH) GENENTECH INC.

XX Devaux B, Keller G, Koeppen H, Lasky LA;

XX WPI; 2001-389954/41.

XX Novel anti-prostate stem cell antigen (PSCA) antibody that internalizes
 on binding to PSCA on mammalian cell and inhibits growth of
 PSCA-expressing cancer cells in vivo, useful for killing
 PSCA-expressing cancer cells -

XX Claim 5; Fig 13; 112pp; English.

XX The present chimeric sequence is full length 2403 immunoglobulin G (IgG)
 antibody heavy chain (5F2.4H4.1E3) derived from murine heavy chain
 variable region (VL) and human IgG heavy chain constant region.
 CC This antibody binds to prostate stem cell antigen (PSCA) which is a
 CC single subunit glycoprotein that is expressed on the cell surface as a
 CC glycosylphosphatidylinositol (GPI)-anchored protein. The present
 CC invention relates to anti-PSCA antibody composition and methods of
 CC killing PSCA-expressing cancer cells. PSCA is useful for inhibiting and
 CC killing the growth of PSCA-expressing cancer cells such as prostate
 CC cancer, bladder cancer or lung cancer cells. Humanised antibody
 CC conjugated to a toxin or a radioactive isotope is used for killing the
 CC cancer cells. PSCA is useful for specifically targeting PSCA-expressing
 CC tumour cells in vivo and for inhibiting or killing these cells. The
 CC antibodies are also useful for treating the above mentioned cancers and
 CC for diagnosing and staging of PSCA-expressing cancer, for purification
 CC or immunoprecipitation of PSCA from cells, and for detection and
 CC quantitation of PSCA in vitro. PSCA DNA is also useful for treating
 CC cancers by gene therapy techniques.

XX Sequence 466 AA;

Query Match 90.5%; Score 2275; DB 22; Length 466;
 Best Local Similarity 90.9%; Pred. No. 8.9e-129;
 Matches 427; Conservative 17; Mismatches 22; Indels 4; Gaps 1;

Qy 1 MGWSCIIILFLVATATGVHSQVQLVSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAP 60

Db 1 mgwsciiilflvatatgvhsqvlvsgaevkpgasvksckasgytftsygmnwvrqap 60

Qy 61 GORLEWMEIDPSDSTYNYNQKFKGKATLTVDTSASTAYMELSLRSEDATVYYCARNRD 120

Db 61 g99lewmgwintygeptygedfkgfafsidsastaymelslrseidatavycar--- 120

Qy 121 YSNNMWYFDVWGEGLVTVSSASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPTVTS 180

Db 121 ysnnmwyfdvwmgeglvtvssastkgpsvfplapskstsggtaalgclvkdyfpeptvts 176

Qy 181 WNSGALTSVHTFPFAVLQSSGLYSLSSVTVTPSSSLGTQTYICNNHKNPSNTKVDKRVPEP 240

Db 177 wnsгалtsгvhtfpavliqssglyslssvttvpssslgtqtyicnnhkpntkvdkkvpep 236

Qy 241 KSCDKHTCCPPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300

Db 237 kscdkhtccppcpapellggpsvflppkpkdtlmisrtpevtcvvdvshedpevkfnw 296

Qy 301 YVDGVEVHNNAKTPREEQYNSTYRVWSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTIS 360

Db 297 yvdgvevhnaktpreeqynstyrvwsvltvlhqdwlngkeyckvsnkalpapiektis 356

QY 361 KAKGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
Db 357 kagqprepqvylpppreemtknqvsltcclvkgfypsdiavewesngqpennykttpv 416
QY 421 LDSGSGFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPCK 470
Db 417 ldsdgsfflyskltvdksrwqgnvfscsvmhealhnhytqkslsispck 466

Search completed: April 24, 2002, 15:09:54
Job time: 97 sec

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OM protein - protein search, using sw model

Run on: April 24, 2002, 15:10:41 ; Search time 42.08 Seconds
(without alignments)
251.344 Million cell updates/sec

Title: US-09-499-662-89

Perfect score: 2515
Sequence: 1 MGWSCILFLVATATGVHSQ.....MHEALHNHYTKSLSPGK 470

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues
Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_patents_AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2216	88.1	449	1	US-08-458-516-13
2	2214	88.0	476	2	US-08-378-939-10
3	2195.5	87.3	467	4	US-09-049-672A-8
4	2189.5	87.1	452	3	US-09-027-449-71
5	2189.5	87.1	452	4	US-09-026-985-71
6	2155.5	85.7	454	2	US-07-934-373C-22
7	2155.5	85.7	454	3	US-08-437-642B-22
8	2155.5	85.7	454	5	PCT-US93-07832-22
9	2113	84.0	451	2	US-08-887-352B-14
10	2113	84.0	451	2	US-08-887-352B-16
11	2113	84.0	451	3	US-08-466-151-65
12	2113	84.0	451	4	US-09-109-207C-14
13	2113	84.0	451	4	US-09-109-207C-16
14	2113	84.0	451	4	US-09-296-005-14
15	2113	84.0	451	4	US-09-296-005-16
16	2110	83.9	478	3	US-08-487-550-8
17	2105	83.7	451	2	US-08-887-352B-18
18	2105	83.7	451	4	US-09-109-207C-18
19	2105	83.7	451	4	US-09-282-505-2
20	2105	83.7	451	4	US-09-054-255-2
21	2105	83.7	451	4	US-09-296-005-18
22	2094	83.3	453	3	US-08-466-151-8
23	2087.5	83.0	467	2	US-07-916-098A-45
24	2083.5	82.8	552	5	PCT-US93-07832-23
25	2080.5	82.7	469	2	US-07-934-373C-23
26	2080.5	82.7	469	3	US-08-437-642B-23
27	2079.5	82.7	459	1	US-08-157-101A-7

28	2061.5	82.0	467	1	US-08-704-744-81	Sequence 81, Appl
29	2059.5	81.9	473	4	US-09-049-672A-4	Sequence 4, Appl
30	2047.5	81.4	445	4	US-08-341-560B-17	Sequence 17, Appl
31	2046	81.4	476	3	US-08-487-550-12	Sequence 12, Appl
32	2043.5	81.3	446	3	US-08-397-411-7	Sequence 7, Appl
33	2014	80.1	476	3	US-08-487-550-4	Sequence 4, Appl
34	2006	79.8	442	5	PCT-US96-10043-9	Sequence 9, Appl
35	1994	79.3	442	1	US-08-461-968A-5	Sequence 5, Appl
36	1994	79.3	442	2	US-08-462-571-5	Sequence 5, Appl
37	1979.5	78.7	450	2	US-08-788-800-12	Sequence 12, Appl
38	1970	78.3	442	1	US-08-480-036-2	Sequence 2, Appl
39	1970	78.3	442	1	US-08-461-968A-2	Sequence 2, Appl
40	1970	78.3	442	2	US-08-462-571-2	Sequence 2, Appl
41	1970	78.3	442	5	PCT-US96-10043-12	Sequence 12, Appl
42	1937	77.0	443	5	PCT-US96-13152-4	Sequence 4, Appl
43	1867.5	74.3	467	4	US-08-523-894-12	Sequence 12, Appl
44	1866.5	74.2	467	4	US-08-523-894-8	Sequence 8, Appl
45	1859.5	73.9	467	4	US-08-523-894-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-458-516-13
; Sequence 13, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-458-516-13

Query Match 88.1%; Score 2216; DB 1; Length 449;
Best Local Similarity 92.5%; Pred. No. 2.5e-164;
Matches 417; Conservative 15; Mismatches 17; Indels 2; Gaps 2;

QY 20 QVOLVOSGAEVKKPGASVSKASGYTFTSYMMOMVKQAPQORLEWMEIDPDSYNTY 79
Db 1 QVOLVOSGAEVKKPGSSVSKASGYAFTNLYIEWVRQAPQGLEWIVPGSGGTNY 60
QY 80 NOKFKGKATLTVDTSASTAYMELSSLSRSDTAVYYCARNRDYSNNWYEDVWEGTLTVTS 139
Db 61 NEKFKGRVLTVDSTNTAYMELSSLSRSDTAVYFCAR-RDGNYGW-FAYWGGTLTVTS 118
QY 140 SASTKGPSVFPLAPSKSTSGTAAALGCLVGDYFPEPVTVSNNSGALTSVGVHTFFAVLOS 199
Db 119 SASTKGPSVFPLAPSKSTSGTAAALGCLVGDYFPEPVTVSNNSGALTSVGVHTFFAVLOS 178
QY 200 SGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVKPCDKTHTCCPCPAPELLG 259
Db 179 SGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVKPCDKTHTCCPCPAPELLG 238
QY 260 GPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDDEVKFNWTVGDVEVHNATKPREEQY 319
Db 239 GPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDDEVKFNWTVGDVEVHNATKPREEQY 298
QY 320 NSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKISKAKGPREPOVYTLPPSRE 379
Db 299 NSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKISKAKGPREPOVYTLPPSRE 358
QY 380 EMTKNQVSLTCLVKGFPSPDI AVEWESNGQPNNTKTPPVLDSDGSEFFLYSKLTVDKSR 439
Db 359 ELTKNQVSLTCLVKGFPSPDI AVEWESNGQPNNTKTPPVLDSDGSEFFLYSKLTVDKSR 418
QY 440 WQGNVFCSCVMHEALHNHYTKSLSLSPGK 470
Db 419 WQGNVFCSCVMHEALHNHYTKSLSLSPGK 449

RESULT 2
US-08-378-939-10
; Sequence 10, Application US/08378939
; Patent No. 5876361
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/378,939
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-378-939-10
Query Match 88.0%; Score 2214; DB 2; Length 476;
Best Local Similarity 87.8%; Pred. No. 3.8e-164;
Matches 418; Conservative 22; Mismatches 30; Indels 6; Gaps 1;
QY 1 MGWSCIILFLVATATGVHISOVOLVOSGARVKKPGASVKYCKSKASGYTFTSYMMOMVKQAP 60
Db 1 MDWTWRFLLFVVAALAGVQSMQVQSGAEVKKPGSSVTVSKKASGTFSNYAIISWRQAP 60
QY 61 GORLEWMEIDPDSYNTYINQKFKGKATLTVDTSASTAYMELSSLSRSDTAVYYCARNR- 119
Db 61 GORLEWMEIGIIPLECTPIYSQNFQGRVTITADKSTSTAHMELTSLRSEDVAVYCATDRY 120
QY 120 -----DYSNNWYEDVWEGTLTVTSASATKGPSVFLPAPSSKSTSGTAAALGCLVGDYFP 174
Db 121 ROANFDRARVGFDPWGGTTLTVSSASTKGPSVFLPAPSSKSTSGTAAALGCLVGDYFP 180
QY 175 EPTVTVSNNSGALTSVGVHTFFAVLOSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKV 234
Db 181 EPTVTVSNNSGALTSVGVHTFFAVLOSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKV 240
QY 235 DKRVKPKCDKTHTCPCPAPELLGSPSVFLPAPSSKSTSGTAAALGCLVGDYFP 294
Db 241 DKRVKPKCDKTHTCPCPAPELLGSPSVFLPAPSSKSTSGTAAALGCLVGDYFP 300
QY 295 EVKFNWYVDGVEVHNATKPREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAP 354
Db 301 EVKFNWYVDGVEVHNATKPREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAP 360
QY 355 IEXTISKAKGPREPOVYTLPPSREMTKNQVSLTCLVKGFPSPDI AVEWESNGQPNNTY 414
Db 361 IEXTISKAKGPREPOVYTLPPSREMTKNQVSLTCLVKGFPSPDI AVEWESNGQPNNTY 420
QY 415 KTTTPVLDSDGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSLSPGK 470
Db 421 KTTTPVLDSDGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSLSPGK 476
RESULT 3
US-09-049-672A-8
; Sequence 8, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:

APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ceirone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGTU11
CLONE: 2747531
US-09-049-672A-8

Query Match 87.3%; Score 2195.5; DB 4; Length 467;
Best Local Similarity 89.0%; Pred. No. 1e-162;
Matches 413; Conservative 20; Mismatches 28; Indels 3; Gaps 1;

QY 7 ILFLVATATGHSOVQLVQSGAEVKKPGASVKVSKASGYFTFTSYMMQWVKQAPQORLEW 66
DB 7 ILFLVATATGHSOVQLVQSGAEVKKPGASVQVSCVTSGFTLSDLVHVVWVKQAPQORLEW 66
QY 67 MGEIDPSDSYNNQKFKGKATLVDTASATYAMLSRLSEDPAVYICARNRDYNNWY 126
DB 67 MGLAPENGAEVYAKELGRLTLEDSTADTAYMFLNLSGSEDAIYYCARQH--YDFE 123
QY 127 FDVWGEGLTVVSSASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSWNSGAL 186
DB 124 FDFWQGTMTVTVSSASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSWNSGAL 183
QY 187 TSGVHTFPVQLQSLVSLVTVPSSSLGTQYICNVNHNKPSNTKVDKRVKPKSCDKT 246
DB 184 TSGVHTFPVQLQSLVSLVTVPSSSLGTQYICNVNHNKPSNTKVDKRVKPKSCDKT 243
QY 247 HTCCPPAPPELLGSPSVFLPPPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVE 306
DB 244 HTCCPPAPPELLGSPSVFLPPPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVE 303
QY 307 VHNKATPREEQYNSTYRVVSVTLVHLDWLNKGYCKVSNKALPAPIEKTISKAKGQP 366
DB 304 VHNKATPREEQYNSTYRVVSVTLVHLDWLNKGYCKVSNKALPAPIEKTISKAKGQP 363
QY 367 REPOVYTLPPSREEMTKNOVSLTCLVKGFPSPDIKAVWESNGQPNKYKTPPVLDSDGS 426
DB 364 REPOVYTLPPSREEMTKNOVSLTCLVKGFPSPDIKAVWESNGQPNKYKTPPVLDSDGS 423
QY 427 FFYLSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 470
DB 424 FFYLSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 467

RESULT 4
US-09-027-449-71
Sequence 71, Application US/09027449
Patent No. 6025158
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way

CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-027-449-71

Query Match 87.1%; Score 2189.5; DB 3; Length 452;
Best Local Similarity 89.6%; Pred. No. 2.8e-162;
Matches 405; Conservative 28; Mismatches 18; Indels 1; Gaps 1;

QY 20 QVQLVQSGAEVKKPGASVKVSKASGYFTFTSYMMQWVKQAPQORLEWGEIDPDSYNNY 79
DB 1 EVQLVQSGGGVLPQGGSLRLSCAASGYFSFSSHHVWVKQAPQORLEWGYIDPSNGETTY 60
QY 80 NQKFKGKATLVDTASATYAMLSRLSEDPAVYICAR-NRDYNNWYFDVWGEGLTVV 138
DB 61 NQKFKGKATLVDTASATYAMLSRLSEDPAVYICAR-NRDYNNWYFDVWGEGLTVV 120
QY 139 SSASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAVLQ 198
DB 121 SSASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAVLQ 180
QY 199 SSGLYSLSSVTVPSSSLGTQYICNVNHNKPSNTKVDKRVKPKSCDKTHTCCPPAPELL 258
DB 181 SSGLYSLSSVTVPSSSLGTQYICNVNHNKPSNTKVDKRVKPKSCDKTHTCCPPAPELL 240
QY 259 GGPSVFLPPPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 318
DB 241 GGPSVFLPPPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 300
QY 319 YNSTYRVVSVTLVHLDWLNKGYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 378
DB 301 YNSTYRVVSVTLVHLDWLNKGYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 360
QY 379 EEMTKNOVSLTCLVKGFPSPDIKAVWESNGQPNKYKTPPVLDSDGSFFLYSKLTVDKS 438
DB 361 EEMTKNOVSLTCLVKGFPSPDIKAVWESNGQPNKYKTPPVLDSDGSFFLYSKLTVDKS 420
QY 439 RWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 470
DB 421 RWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 452

RESULT 5
US-09-026-985-71

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; Sequence 71, Application US/09026985
; Patent No. 6133426
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,985
; FILING DATE: 20-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: PI085R3-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-026-985-71

Query Match      87.1%; Score 2189.5; DB 4; Length 452;
Best Local Similarity 89.6%; Pred. No. 2.8e-162;
Matches 405; Conservative 28; Mismatches 18; Indels 1; Gaps 1;

Qy 20 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYVMQWVKQAPGQRLNWMGEIDPDSSTNY 79
Db 1 EVQLVQSGGGLVQPGGSRLLSCAASGYFSFSSHYMHWVRKAPGKGLWVGYYIDPSNGET 60
Qy 80 NQKFKGKATLVDTVSASTAYMELSLRSEDYAVYYCAR-NRDYSNNWYFDVWGEGTLTV 138
Db 61 NQKFKGRTLSRDNSKNTAYLQMSLRADYAVYYCARGDYRNGDWFDFVWGQGLTV 120
Qy 139 SSASTKGSVPFLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 198
Db 121 SSASTKGSVPFLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 180
Qy 199 SSGLYSLSSVTVTPSSSLGTQYICNVNHPKSNTKVDKRVKPEKSCDKTHTCPPCPAPELL 258
Db 181 SSGLYSLSSVTVTPSSSLGTQYICNVNHPKSNTKVDKRVKPEKSCDKTHTCPPCPAPELL 240
Qy 259 GGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 318
Db 241 GGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 300
Qy 319 YNSTYRVVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSR 378
Db 301 YNSTYRVVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSR 360
Qy 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPTPVLDSDGSFFLYSKLTVDK 438
Db 361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPTPVLDSDGSFFLYSKLTVDK 420
Qy 439 RWQOGNVFSCSMHEALHNHYTQKSLSLSPGK 470
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Db 421 RWQOGNVFSCSMHEALHNHYTQKSLSLSPGK 452

RESULT 6
US-07-934-373C-22
; Sequence 22, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/115272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-22
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Query Match      85.7%; Score 2155.5; DB 2; Length 454;
Best Local Similarity 89.2%; Pred. No. 1.2e-159;
Matches 405; Conservative 17; Mismatches 29; Indels 3; Gaps 1;
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Qy 20 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYVMQWVKQAPGQRLNWMGEIDPDSSTNY 79
Db 1 QVQLVQSGPELVKPGASVKISCKTSGYFTTEYTHHWKQSHGKSLWLGGENPKNNGSSH 60
Qy 80 NQKFKGKATLVDTVSASTAYMELSLRSEDYAVYYCARNRDYSNNW---YFDVWGEGTLV 136
Db 61 NQRFMDKATLAVDKSTSTAYMELSLTSEDSGIYVCARWRLNGYGFDRYRFDVWGAGTV 120
Qy 137 TVSSASTKGSVPFLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 196
Db 121 TVSSASTKGSVPFLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 180
Qy 197 LQSGLYSLSSVTVTPSSSLGTQYICNVNHPKSNTKVDKRVKPEKSCDKTHTCPPCPAPE 256
Db 181 LQSGLYSLSSVTVTPSSSLGTQYICNVNHPKSNTKVDKRVKPEKSCDKTHTCPPCPAPE 240
Qy 257 LLGSPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 316
Db 241 LLGSPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 300
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Qy	317	EQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPPVYTLLP	376
Db	301	EQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPPVYTLLP	360
Qy	377	SREEMTKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVD	436
Db	361	SREEMTKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVD	420
Qy	437	KSRWQOGNFSCSYMHEALHNHYTQKSLSLSPCK	470
Db	421	KSRWQOGNFSCSYMHEALHNHYTQKSLSLSPCK	454

RESULT 7
US-08-437-642B-22
Sequence 22, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437.642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709p2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: Amino acid
TOPOLOGY: Linear
US-08-437-642B-22

	Query Match	85.7%	Score 2155.5	DB 3	Length 454
	Best Local Similarity	89.3%	Pred. No. 1.2e-159		
	Matches 405	Conservative 17	Mismatches 29	Indels 3	Gaps 1
QY	20	QVQLVQSGAEVKKPGASVKVSCKASGYFTFTSYNMQWVKQAPGORLEWMEIDPDSYTN	79		
DB	1	QVQLVQSGPELVKPGASVKISCKTSGYFTFTYTHMMHMQSKGKLEWIGTFGNPKNGGSSH	60		

```

01 QY 80 NQFKGKATLTVDTISASTAYMEISSLRSEDYAVYYCARNRDYNNW---YFDVWGBGTLV 130
02      ||: || || || || || || || || || || || || || || || || || || || || ||
03 Db 61 NQRFMDKATLAVDKSTSTAYMEISSLRSLTSEDGIIYYCARNRGLNYGFDVRYFDVWAGATTV 120
04
05 QY 137 TVSSASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 196
06      || || || || || || || || || || || || || || || || || || || || || || ||
07 Db 121 TVSSASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 180
08
09 QY 197 LQSSGLYSLSSVTVFPSSSLGTQTYICNVNHNKPSNTKVDKRKVEPKSCDKTHTCCPPCPAPE 256
10      || || || || || || || || || || || || || || || || || || || || || || ||
11 Db 181 LQSSGLYSLSSVTVFPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCCPPCPAPE 240
12
13 QY 257 LLGSPSVFLPPPKPKDTLMSRTPETVCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPRE 316
14      || || || || || || || || || || || || || || || || || || || || || || ||
15 Db 241 LLGSPSVFLPPPKPKDTLMSRTPETVCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPRE 300
16
17 QY 317 EQNSTYRVVSVLTVLHODMNLGKEYCKKVSNAKALPAPTEKTSKAKGQPREPQVYTLPP 376
18      || || || || || || || || || || || || || || || || || || || || || || ||
19 Db 301 EQNSTYRVVSVLTVLHODMNLGKEYCKKVSNAKALPAPTEKTSKAKGQPREPQVYTLPP 360
20
21 QY 377 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVD 436
22      || || || || || || || || || || || || || || || || || || || || || || ||
23 Db 361 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVD 420
24
25 QY 437 KSRWQGNVFPSCSYMHEALHNHYTQKSLSLSPGK 470
26      || || || || || || || || || || || || || || || || || || || || || || ||
27 Db 421 KSRWQGNVFPSCSYMHEALHNHYTQKSLSLSPGK 454
28
29 RESULT 8
30 PCI-US93-07832-22
31 ; Sequence 22, Application PC/TUS9307832
32 ; GENERAL INFORMATION:
33 ; APPLICANT: Genentech, Inc.
34 ; TITLE OF INVENTION: Immunoglobulin Variants
35 ; NUMBER OF SEQUENCES: 40
36 ; CORRESPONDENCE ADDRESS:
37 ; ADDRESSEE: genentech, Inc.
38 ; STREET: 460 Point San Bruno Blvd
39 ; CITY: South San Francisco
40 ; STATE: California
41 ; COUNTRY: USA
42 ; ZIP: 94080
43 ;
44 ; COMPUTER READABLE FORM:
45 ; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
46 ; COMPUTER: IBM PC compatible
47 ; OPERATING SYSTEM: PC-DOS/MS-DOS
48 ; SOFTWARE: patin (Genentech)
49 ; CURRENT APPLICATION DATA:
50 ; APPLICATION NUMBER: PCT/US93/07832
51 ; FILING DATE: 19930820
52 ; CLASSIFICATION:
53 ; PRIOR APPLICATION DATA:
54 ; APPLICATION NUMBER: 07/715272
55 ; FILING DATE: 14-JUN-1991
56 ; PRIOR APPLICATION DATA:
57 ; APPLICATION NUMBER: PCT/US92/05126
58 ; FILING DATE: 15-JUN-1992
59 ; PRIOR APPLICATION DATA:
60 ; APPLICATION NUMBER: 07/934373
61 ; FILING DATE: 21-AUG-1992
62 ; ATTORNEY/AGENT INFORMATION:
63 ; NAME:
64 ; REGISTRATION NUMBER:
65 ; REFERENCE/DOCKET NUMBER: 709P2PCT
66 ; TELECOMMUNICATION INFORMATION:
67 ; TELEPHONE:
68 ; TELEFAX: 415/952-9881
69 ; TELEX: 910/371-7168
70 ; INFORMATION FOR SEQ ID NO: 22:
71 ; SEQUENCE CHARACTERISTICS:
72 ; LENGTH: 454 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
PCT-US93-07832-22

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Query Match	85.7%;	Score 2155.5;	DB 5;	Length 454;
Best Local Similarity	89.2%;	Pred. No. 1.2e-159;		
Matches 405;	Conservative 17;	Mismatches 29;	Indels 3;	Gaps 1;


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; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-14

Query Match      84.0%; Score 2113; DB 4; Length 451;
Best Local Similarity 87.2%; Pred. No. 2.4e-156;
Matches 394; Conservative 25; Mismatches 31; Indels 2; Gaps 2;

Qy 20 QVLVQSGAEYKKPGASVKVCKASGYTFTS-YMQWVKVQAPGORLEWNGEIDPSDSYTN 78
Db 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNWIRQAPGKLEWVASI-TYDGSN 59
Qy 79 YNQRFKGKATLVDTASTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGEGTLTV 138
Db 60 YNPVKGRITISRDTSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVMGQGLTV 119
Qy 139 SSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQ 198
Db 120 SSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQ 179
Qy 199 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKRVPEKSCDKTHTCCPPAPPELL 258
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKRVPEKSCDKTHTCCPPAPPELL 239
Qy 259 GGSVFLFPPPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQ 318
Db 240 GGSVFLFPPPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQ 299
Qy 319 YNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
Db 300 YNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359
Qy 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKS 438
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKS 419
Qy 439 RWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
Db 420 RWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 13
US-09-109-207C-16
; Sequence 16, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
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; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-16

Query Match      84.0%; Score 2113; DB 4; Length 451;
Best Local Similarity 87.2%; Pred. No. 2.4e-156;
Matches 394; Conservative 25; Mismatches 31; Indels 2; Gaps 2;

Qy 20 QVLVQSGAEYKKPGASVKVCKASGYTFTS-YMQWVKVQAPGORLEWNGEIDPSDSYTN 78
Db 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNWIRQAPGKLEWVASI-TYDGSN 59
Qy 79 YNQRFKGKATLVDTASTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGEGTLTV 138
Db 60 YNPVKGRITISRDTSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVMGQGLTV 119
Qy 139 SSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQ 198
Db 120 SSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQ 179
Qy 199 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKRVPEKSCDKTHTCCPPAPPELL 258
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKRVPEKSCDKTHTCCPPAPPELL 239
Qy 259 GGSVFLFPPPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQ 318
Db 240 GGSVFLFPPPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQ 299
Qy 319 YNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
Db 300 YNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359
Qy 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKS 438
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKS 419
Qy 439 RWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
Db 420 RWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 14
US-09-296-005-14
; Sequence 14, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-14

Query Match      84.0%; Score 2113; DB 4; Length 451;
Best Local Similarity 87.2%; Pred. No. 2.4e-156;
Matches 394; Conservative 25; Mismatches 31; Indels 2; Gaps 2;

Qy 20 QVLVQSGAEYKKPGASVKVCKASGYTFTS-YMQWVKVQAPGORLEWNGEIDPSDSYTN 78
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```
Db 1 EVQLVESGGGLVQPGGSLRLSCAVGSYITSGYSNWIRQAPGKGLEWVAST-TYDGSIN 59
Qy 79 YNOKFKGKATLTVDTSASTAYMELSSLRSEDTAVYICARNRDYSNNWYFDVWGEGTLTV 138
Db 60 YNPSVKGRITISRDSDSKNTFYLQNSLRAEDTAVYICARGSHYFGHWFHFAVWGQTLTV 119
Qy 139 SSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 198
Db 120 SSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 179
Qy 199 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKRVKPKSCDKTHTCPPCPAPELL 258
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKRVKPKSCDKTHTCPPCPAPELL 239
Qy 259 GGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 318
Db 240 GGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299
Qy 319 YNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
Db 300 YNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359
Qy 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKS 438
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKS 419
Qy 439 RWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 470
Db 420 RWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 451
```

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RESULT 15
US-09-296-005-16
; Sequence 16, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123clr
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-16
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Query Match 84.0%; Score 2113; DB 4; Length 451;
Best Local Similarity 87.2%; Pred. No. 2.4e-156;
Matches 394; Conservative 25; Mismatches 31; Indels 2; Gaps 2;

Qy 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YHWQWVKAPQGORLEMMGEIDFSDSYTN 78
Db 1 EVQLVESGGGLVQPGGSLRLSCAVGSYITSGYSNWIRQAPGKGLEWVAST-TYDGSIN 59
Qy 79 YNOKFKGKATLTVDTSASTAYMELSSLRSEDTAVYICARNRDYSNNWYFDVWGEGTLTV 138
Db 60 YNPSVKGRITISRDSDSKNTFYLQNSLRAEDTAVYICARGSHYFGHWFHFAVWGQTLTV 119
Qy 139 SSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 198
Db 120 SSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 179
Qy 199 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKRVKPKSCDKTHTCPPCPAPELL 258
```

```
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKRVKPKSCDKTHTCPPCPAPELL 239
Qy 259 GGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 318
Db 240 GGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299
Qy 319 YNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
Db 300 YNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359
Qy 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKS 438
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKS 419
Qy 439 RWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 470
Db 420 RWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 451
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Search completed: April 24, 2002, 15:10:42
Job time: 145 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 15:11:37 ; Search time 49.97 Seconds
(without alignments)
716.471 Million cell updates/sec

Title: US-09-499-662-89
Perfect score: 2515
Sequence: 1 MOWSILFLVATATGVHSQ.....MHEALNNHYTQKSLSLSPGK 470

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1758	69.9	330	GHU	Ig gamma-1 chain C
2	1639.5	65.2	377	A23511	Ig gamma-3 chain C
3	1637.5	65.1	377	A60764	Ig gamma-3 chain C
4	1610	64.0	326	G2HU	Ig gamma-2 chain C
5	1602.5	63.7	469	S37483	Ig gamma-2a chain C
6	1599.5	63.6	327	G4HU	Ig gamma-4 chain C
7	1538	61.2	474	G2MS11	Ig gamma-2b chain C
8	1536	61.1	446	S40295	Ig gamma-2a chain C
9	1493.5	59.4	475	S01321	Ig gamma-2b chain C
10	1470	58.4	470	S22080	Ig heavy chain pre
11	1466	58.3	472	S31459	Ig gamma-1 chain -
12	1439.5	57.2	444	PC4436	monoclonal antibod
13	1428	56.8	374	S69339	Ig heavy chain v r
14	1267	50.4	328	I47159	Ig gamma 2a chain
15	1261	50.1	328	I47160	Ig gamma 2b chain
16	1253	49.8	255	S31866	Ig gamma-1 chain C
17	1245	49.5	234	PT0207	Ig gamma chain C r
18	1235	49.1	328	I47158	Ig gamma 1 chain C
19	1231.5	49.0	323	GHRB	Ig gamma chain C r
20	1231	48.9	328	I47161	Ig gamma 3 chain C
21	1210.5	48.1	329	G2GP	Ig gamma-2 chain C
22	1165.5	46.3	308	S30554	Ig heavy chain C r
23	1157	46.0	289	G3HWT	Ig gamma-3 heavy C
24	1155	45.9	326	PS0017	Ig gamma-1 chain C
25	1150	45.7	329	G3MSC	Ig gamma-3 chain C
26	1145	45.5	324	G1MS	Ig gamma-1 chain C
27	1144.5	45.5	333	PS0018	Ig gamma-2b chain C
28	1140	45.3	393	G1MSM	Ig gamma-1 chain C
29	1139	45.3	398	G3MSM	Ig gamma-3 chain C

30 1129 44.9 330 1 G2MSA
31 1127.5 44.8 329 2 S00847
32 1126.5 44.8 335 1 G2MSAB
33 1124 44.7 399 1 G2MSAM
34 1115 44.3 322 2 PS0019
35 1093.5 43.5 327 2 S06611
36 1080 42.9 405 1 G2MSBM
37 1070 42.5 277 2 I47162
38 1000 39.8 548 2 S38864
39 927 36.9 627 2 S14683
40 914.5 36.4 549 2 S04845
41 860.5 34.2 241 2 S69131
42 843 33.5 246 2 S38950
43 787 31.3 220 2 A49444
44 751.5 29.9 249 2 S69340
45 751.5 29.9 572 2 B46529

ALIGNMENTS

RESULT 1

CHHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C:Accession: A93433; S36861; S38887; B90563; A90564; B91668; A91723; A02146
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <ELL>

A:Cross-references: EMBL:Z17370

A:Note: This sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) marker

A:Note: Lys-330 is removed after translation

R:Harris, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution

A:Reference number: S33887; MUID:83001943

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113;235-330 <TAK>

A:Cross-references: EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelm

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid se

A:Reference number: A90563; MUID:71064024

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96, R',98-135 <CUN>

A:Note: This sequence has the G1m(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid s

A:Reference number: A90564; MUID:71064025

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154, Q',156-165, Q',167-176, Q',178-194, N',196-197, D',199-238, E',

A:Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met

R:Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's z. Physiol. Chem. 357, 1571-1604, 1976

A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein t

igen Primaerstruktur.

A:Reference number: A91668; MUID:77070269
A:Contents: myeloma protein Nie
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A:Note: this sequence has the G1m(17) and G1m(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOI
A:Reference number: A91723; MUID:83289131
A:Contents: myeloma protein KOL; disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A:Note: this sequence has the G1m(3) and G1m(non-1) markers
R:Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A:Reference number: A90565; MUID:71064027
A:Contents: annotation; disulfide bonds
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267
A:Contents: annotation; disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG1
A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 114/1; 224/1
A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:20-85/Domain: immunoglobulin homology <IM1>
F:137-206/Domain: immunoglobulin homology <IM2>
F:243-310/Domain: immunoglobulin homology <IM3>
F:27-83,144-204,250-308/Disulfide bonds: #status experimental
F:103/Disulfide bonds: interchain (to light chain) #status experimental
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 69.9%; Score 1758; DB 1; Length 330;
Best Local Similarity 99.1%; Pred. No. 7.9e-94;
Matches 327; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 200
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Qy 201 GLYSLSVVTVPSSSLGQTGYTCNVNHPKSNTKVDKRVKSCDKTHTCPPCPAPPELLGG 260
Db 61 GLYSLSVVTVPSSSLGQTGYTCNVNHPKSNTKVDKRVKSCDKTHTCPPCPAPPELLGG 120
Qy 261 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320
Db 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Qy 321 STYRVSVTLTVLQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRREE 380
Db 181 STYRVSVTLTVLQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 240
Qy 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 440
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300
Qy 441 QGQNVFSCSVMHREALHNYHTQKSLSPGK 470
Db 301 QGQNVFSCSVMHREALHNYHTQKSLSPGK 330

RESULT 2

Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
A:Accession: A23511
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene:
A:Reference number: A23511; MUID:86148507
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 65.2%; Score 1639.5; DB 2; Length 377;
Best Local Similarity 82.8%; Pred. No. 5.5e-87;
Matches 312; Conservative 7; Mismatches 11; Indels 47; Gaps 1;

Qy 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 200
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Qy 201 GLYSLSVVTVPSSSLGQTGYTCNVNHPKSNTKVDKRVKSCDKTHTCPPCPAPPELLGG 238
Db 61 GLYSLSVVTVPSSSLGQTGYTCNVNHPKSNTKVDKRVKSCDKTHTCPPCPAPPELLGG 120
Qy 239 -----EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKPKDT 273
Db 121 DTPPPCPKPCPEPKSCDTTPPCPCPEPKSCDTTPPCPCPEPKSCDTTPPCPCPEPKPKDT 180
Qy 274 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLH 333
Db 181 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLH 240
Qy 334 QDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDEMTKNQVSLTCLVK 393
Db 241 QDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDEMTKNQVSLTCLVK 300
Qy 394 GFYPDSIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSVMH 453
Db 301 GFYPDSIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSVMH 360
Qy 454 ALHNHYTQKSLSLSPGK 470
Db 361 ALHNHYTQKSLSLSPGK 377

RESULT 3

Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
A:Accession: A60764
R:Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 con
A:Reference number: A60764; MUID:90007613
A:Accession: A60764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

```
Query Match      65.1%; Score 1637.5; DB 2; Length 377;
Best Local Similarity 82.8%; Pred. No. 7.2e-87;
Matches 312; Conservative 7; Mismatches 11; Indels 47; Gaps 1;

QY 141 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200
Db 1 ASTKGPSVFLPAPCSRSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

QY 201 GLYSLSSVTVPSSSLGTYICNVNHNKPSNTKVDKRV----- 238
Db 61 GLYSLSSVTVPSSSLGTYICNVNHNKPSNTKVDKRVKELKPLDGTHTTCRCRCPKSC 120

QY 239 -----EPKSCDKTHTCCPCPAPPELLGGPSVFLPPPKPDT 273
Db 121 DTPPPCPCRPKSCDTPPCRCPEKSCDTPPCPCPAPPELLGGPSVFLPPPKPDT 180

QY 274 LMSRTPETVTVVVDVSHEDPEVKFNWYVDGVEVHNKTPRPEQYNSTYRVVSVLTVHL 333
Db 181 LMSRTPETVTVVVDVSHEDPEVQFNWYVDGVEVHNKTPRPEQYNSTYRVVSVLTVHL 240

QY 334 QDWLNKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTPPPSRDEMTKNQVSLTCLVK 393
Db 241 QDWLNKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTPPPSRDEMTKNQVSLTCLVK 300

QY 394 GFVPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHE 453
Db 301 GFVPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHE 360

QY 454 ALHNHYTQKSLSLSPGK 470
Db 361 ALHNRETQKLSLSPGK 377
```

RESULT 4

G2HU
Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C:Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A:Reference number: A93906; MUID:82197621
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <ELL>
A:Cross-references: GB:V00554; GB:J00230; MID:g32759; PIDN:CAB58438.1; PID:g6066056
A:Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A:Reference number: A92809; MUID:81007873
A:Contents: myeloma protein T11
A:Accession: A92809
A:Molecule type: protein
A:Residues: 1-19, 'Q', 21-57, '2', 59, 'A', 61-193, 'D', 195-325 <NAN>
A:Note: Trp-156 is at or near the complement-binding site
R:Conneally, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A:Title: The amino acid sequences of the three heavy chain constant region domains of a
A:Reference number: A90752; MUID:80001357
A:Contents: myeloma protein Z1e
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, '222', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
A:Note: this sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g

A:Reference number: A93132; MUID:80114419
A:Contents: Z1e
A:Accession: A93132
A:Molecule type: Protein
A:Residues: 238-275 <HOF>
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation; Z1e, revisions to residues 25, 59, 60, and 264-268
A:Note: the revised sequence differs from that shown in having 60-Ala and in the am
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500
A:Contents: annotation; myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-146, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124
A:Contents: annotation; Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG2
A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:133-202/Domain: Immunoglobulin homology <IM2>
F:239-306/Domain: Immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,140-200,246-304/Disulfide bonds: #status experimental
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

```
Query Match      64.0%; Score 1610; DB 1; Length 326;
Best Local Similarity 91.8%; Pred. No. 2.3e-85;
Matches 303; Conservative 10; Mismatches 13; Indels 4; Gaps 2;

QY 141 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200
Db 1 ASTKGPSVFLPAPCSRSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

QY 201 GLYSLSSVTVPSSSLGTYICNVNHNKPSNTKVDKRVKSCDKTHTCCPCPAPPELLGG 260
Db 61 GLYSLSSVTVPSSTGTYTCNVNHNKPSNTKVDKRVKSCDKTHTCCPCPAPPELLGG 116

QY 261 PSVFLPFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTPRPEQYN 320
Db 117 PSVFLPFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTPRPEQYN 176

QY 321 STYRVSVLTVLHODWLNKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTPPPSRDE 380
Db 177 STYRVSVLTVLHODWLNKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTPPPSRDE 236

QY 381 MTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 440
Db 237 MTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 296

QY 441 QQQNVFSCSVNHEALHNHYTQKSLSLSPGK 470
Db 297 QQQNVFSCSVNHEALHNHYTQKSLSLSPGK 326
```

RESULT 5

S37483
Ig gamma-2a chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37483

Qy		60	
1	MWSCHIILFLVATATGVHISOVLQSGAEVKKPGASVKYVSCKASGTYTFTSYMHWKQAP	60	
	I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :		
Db	1	MEWSIIFLLSLTAGVHSVQLQQSGPELVNPGASVKMSCKASGYTFITYVMHWKQP	60
	I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :		
Qy	61	GQRLEWMEGLDPSDSYNYNQKFKGATLTVDTSASTAYMELSSLSRSEDFAVYYCARNRD	120
	I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :		
Db	61	GOGLEWIGIYNPKDGTKFNEKEFKRGATLTSDRKSNTAYMELSSLTSEDSAVYYCARDYD	120
	I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :		
Qy	121	YSNNWYFDVWGEGEGLTVITVSAAGTSKGSVPFPPLAPSRSKTSGGTTAALGCLVKDYKPEPVTVS	180
	I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :		
Db	121	YD---WFAYWGQGLTVIVSAAKTPSPSVYPLAPCGDDTTTGSSVYTSGCLKVGYPEPSTVT	177
	I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :		
Qy	181	WNSGALTSGVHTPPAVLQSSGLYSLSSVVTVPPSSSLGTQTYICNVNHKKPSNTKDVRKVEP	240
	I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :		
Db	178	WNSSLSSSVHTLSQAALLQSLGYTMESSVTVPSSTWPQTVCVAHPASSITVDKKLEP	237
	I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :		
Qy	241	KSCDKT-HITCPP-----CPAPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHED	293
	I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :		
Db	238	SGPISTINPCPPCKECKHCAPNLGGGPSVFIEFPPNIKDVMLISLTPTKYTCVVVDISED	297
	I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :		
Qy	294	PEVKFNWYVDCGEVHNAKTKPREEQYNSTYRVYVSVLTLVLDHDLNGKEYCKCVSNKALPA	353

Db 355 EEEMTKKQVLTCTCMVTDPEMPEYIWEVNTNGKTELNYKNTPEVLDSGSGYFMYSKLRVEK 414
QY 438 SRWQOGNVFSCVMHEALHNHYTKSLSPG 469
Db 415 KNNVERNYSVCSVHVEGLHNHHTTKSFSTRPG 446

RESULT 9

S01321
Ig gamma-2b chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
A:Accession: S01321
R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a
A:Reference number: S01320; MUID:88329081
A:Accession: S01321
A:Molecule type: mRNA
A:Residues: 1-475
A:Cross-references: EMBL:X13188; NID:951780; PID:CAA31580.1; PID:951781
A:Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>
F:159-223/Domain: immunoglobulin homology <IMM>

Query Match 59.4%; Score 1493.5; DB 2; Length 475;
Best Local Similarity 60.4%; Pred. No. 1.6e-78;
Matches 288; Conservative 66; Mismatches 114; Indels 9; Gaps 4;

QY 1 MGNSCIIILFVATATGVHSQVLQVSGAEVKKPGASVKVSKASGYTFTSYVMQWVQAP 60
Db 1 MEWIFILFISLTAGVQSQVLOQSGAELARPGASVKLSCKASGYTFTSYGISWVKQRT 60
QY 61 GORLEWMEIDPSDSTYNNQKFKGKATLTVDTSASTAYMELSLRSDEDTAVVYCARNR 120
Db 61 GCGLEWIEIIPGSGNSVFNKFKGKATLTVDKSSSTAYLHLSLTSDESAVYFCAGPRQ 120
QY 121 YSNNNYFDVWGBGTLTVTVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVS 180
Db 121 V-GLLPFGYWGQGLTVTASAAKTPPSVPLAPGCGDITGSSVTLGCLVKGYFPEPSVVT 179
QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKRV 240
Db 180 WNSGLSSSVHTFPALLO-SGLYTMSSSVTVPPSSWPSQTVCVAHPASSTVDKCLEP 238
QY 241 KSCDKT-HTCPP-CPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHED 293
Db 239 SGPTSTINPCPKCHCKCPAPNLEGGSVFIFFPNIKIDVLMISLTPKVTCTVVDVSEDD 298
QY 294 PEVKFNWYVDGVVEVHNATKPREEQNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPA 353
Db 299 PDVQISWFVNNVEVLTAQTQTHREDYNSTIRVVSALPIQHODWMSGKEFKVNNKDLPA 358
QY 354 PIEKTISKAKQPREQVYITLPPSREMTKNQVSLTCLVKGYFSPSDIAVEWESNGQPENN 413
Db 359 PIERTISKIGIVAPQVYIILSPPEQISRKDVSLTCLAVGFSPEIDISVEWTSNGTTEEN 418
QY 414 YKTPPVLDSGSPFLYSKLTVDKSRWQGNVFCVSMHEALHNHYTKSLSPG 470
Db 419 YKDTAPVLDSGSPFIYSKLNKTSKWEKTSFSCNVRHREGLKNLYLKKTSRSPGK 475

RESULT 10

S22080
Ig heavy chain precursor (B/Wt.4A.17.H5.A5) - bovine
N:Alternate names: Ig gamma-1 chain C region (clone 8.10)
C:Species: Bos primigenius taurus (cattle)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S22080; S06610; A31303
R:Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A:Reference number: S22080
A:Accession: S22080
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-470 <SAN>
A:Cross-references: EMBL:X62916; NID:9439; PID:CAA44699.1; PID:9440
R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and
A:Reference number: S06610; MUID:90097956
A:Accession: S06610
A:Molecule type: DNA
A:Residues: 142-470 <SYM>
A:Cross-references: EMBL:X16701
A:Note: the sequence was determined from the germline gene
C:Genetics:
A:Gene: Ig CH gamma-1
A:Introns: 98/1; 111/1; 221/1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: glycoprotein; heterotrimer; immunoglobulin; membrane protein
F:161-225/Domain: immunoglobulin homology <IMM>
F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 58.4%; Score 1470; DB 2; Length 470;
Best Local Similarity 60.0%; Pred. No. 3.6e-77;
Matches 283; Conservative 64; Mismatches 115; Indels 10; Gaps 7;

QY 3 WSCIILFVATATGVHSQVLQVSGAEVKKPGASVKVSKASGYTFTSYVMQWVQAPGQ 62
Db 5 WT--LLFVLSAPIGVLSQVQLRESGPSLVKPSQTLISLCTVSGFSLSSVLTWVQAPGK 62
QY 63 RLEWMEIDPSDSTYNNQKFKGKATLTVDTSASTAYMELSLRSDEDTAVVYCARNR--D 120
Db 63 ALEWVGGI-TSGGTYVNPALKSRLSITKENSQVLSVSVTPEDTATYTCARSTYCE 121
QY 121 YSNNNYFDVWGBGTLTVTVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVS 180
Db 122 VDGAIADAWGGLLTVTVSSASTTAPKVYPLSSCCGDKSSSTVTGLGLVSSYMPPEVTVT 181
QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKRV 240
Db 182 WNSGALKSGVHTFPAVLQSSGLYSLSSVTVPPSGTSG-QTFTCNVAHPASSTKVDKAVDP 240
QY 241 KSCDKTHTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFM 300
Db 241 -TC-KPSPCDCCPPPELPGPSVFIFFPKPKDTLTISGTPEVTCVVDVGVHDPEVKFSW 298
QY 301 YVDGVVEVHNATKPREEQNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAIETKTS 360
Db 299 FVDDVEVNTATKPREEQNSTYRVVSALRIQHODWGTGKEPKCKVHNEGLPAPIVRTIS 358
QY 361 KAKGPPEPQVYITLPPSREMTKNQVSLTCLVKGYFSPSDIAVEWESNGQP--ENNVTKP 418
Db 359 RTKGPAREPQVYITLAPQEEELSKSVSLTCTMTSYFDYIAVEWQNGOPSEDEKYGTP 418
QY 419 PVLDSGSPFLYSKLTVDKSRWQGNVFCVSMHEALHNHYTKSLSPG 470
Db 419 PQLDADSSVFLYSKLRVDRNSWQEGDGTCTVVMHEALHNHYTKSTKSAGK 470

RESULT 11

S31459
Ig gamma-1 chain - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S31459
R:Patric, S.; Nau, F.
submitted to the EMBL Data Library, December 1992
A:Reference number: S31459

[illegible]

QY 182 NSGALTSVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVKRVEPK 241
Db 143 -----EPK 145
QY 242 SCDKTHCPCPAPELLLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY 301
Db 146 SCDKTHCPCPAPELLLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY 205
QY 302 VDGVEVHNKTPREQYNTSTRVSVLVLHQLDNLNGKEYCKVSNKALPAPIERTISK 361
Db 206 VDGVEVHNKTPREQYNTSTRVSVLVLHQLDNLNGKEYCKVSNKALPAPIERTISK 265
QY 362 AKGQPREPOVYITLPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGOPENNYKTTPPV 421
Db 266 AKGQPREPOVYITLPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGOPENNYKTTPPV 325
QY 422 DSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK 470
Db 326 DSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK 374

RESULT 14
147159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845
A:Accession: I47159
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03779; NID:9433123; PID:AAA52217.1; PID:9433124
C:Genetics:
A:Gene: IgG2a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 50.4%; Score 1267; DB 2; Length 328;
Best Local Similarity 69.9%; Pred. No. 9.8e-66;
Matches 232; Conservative 42; Mismatches 52; Indels 6; Gaps 2;
QY 141 ASTKGPSVFLPAPSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 200
Db 1 APKTAPSVYPLAPCSRDTSGPNVALGCLASSYFPEPTVSNWNSGALTSGVHTFPAVLQSS 60
QY 201 GLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVKRVEPKSCDKTHCPCPAPELLGG 260
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVKRVEPKSCDKTHCPCPAPELLGG 320
QY 261 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTPREQYN 320
Db 117 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTPREQYN 176
QY 321 STYRVSVLVLHQLDNLNGKEYCKVSNKALPAPIERTISKAKGQPREPOVYITLPPSREE 380
Db 177 STYRVSVLVLHQLDNLNGKEYCKVSNKALPAPIERTISKAKGQPREPOVYITLPPHAE 236
QY 381 MTKNQVSLTCLVKGFYPSDIAVWESNGO--PENNYKTPPVLDSDGSFFLYSKLTVDKS 438
Db 237 LSRKSVISITCLVIGFYPPDIDVEWQRNGQPEPEGNRTTPPQQDVGDTYLYSKFSVDKA 296
QY 439 RWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
Db 297 SWGGGIFQCAVMHEALHNHYTQKSISKTPGK 328

Search completed: April 24, 2002, 15:11:38
Job time: 196 sec

Ig gamma 2b chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47160
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of
A:Reference number: I47158; MUID:95015845
A:Accession: I47160
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03780; NID:9433125; PID:AAA52218.1; PID:9433126
C:Genetics:
A:Gene: IgG2b
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 50.1%; Score 1261; DB 2; Length 328;
Best Local Similarity 69.6%; Pred. No. 2.2e-65;
Matches 231; Conservative 41; Mismatches 54; Indels 6; Gaps 2;
QY 141 ASTKGPSVFLPAPSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 200
Db 1 APKTAPSVYPLAPCSRDTSGPNVALGCLASSYFPEPTVSNWNSGALTSGVHTFPAVLQSS 60
QY 201 GLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVKRVEPKSCDKTHCPCPAPELLGG 260
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVKRVEPKSCDKTHCPCPAPELLGG 116
QY 261 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTPREQYN 320
Db 117 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTPREQYN 176
QY 321 STYRVSVLVLHQLDNLNGKEYCKVSNKALPAPIERTISKAKGQPREPOVYITLPPSREE 380
Db 177 STYRVSVLVLHQLDNLNGKEYCKVSNKALPAPIERTISKAKGQPREPOVYITLPPHAE 236
QY 381 MTKNQVSLTCLVKGFYPSDIAVWESNGO--PENNYKTPPVLDSDGSFFLYSKLTVDKS 438
Db 237 LSRKSVISITCLVIGFYPPDIDVEWQRNGQPEPEGNRTTPPQQDVGDTYLYSKFSVDKA 296
QY 439 RWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
Db 297 SWGGGIFQCAVMHEALHNHYTQKSISKTPGK 328

Search completed: April 24, 2002, 15:11:38
Job time: 196 sec

RT Intrachain disulfide bonds *;
 RL Biochemistry 9:3188-3196(1970).
 RN [7]
 RP DISULFIDE BONDS.
 RX MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
 RT characterization of the protein, the L- and H-chains, the
 RT cyanogen bromide cleavage products, and the disulfide bridges *;
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=81208100; PubMed=7236608;
 RA Deisenhofer J.;
 RT "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from Staphylococcus
 RT aureus at 2.9- and 2.8-A resolution *;
 RL Biochemistry 20:2361-2370(1981).
 CC -|- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE
 CC MARKER & THE GIM (NON-1) MARKERS.
 CC -|- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
 CC 35,116,198,269 & 272.
 CC -|- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
 CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
 CC 268-272.
 CC -|- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
 CC RESIDUES 198,267&272.
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 DR EMBL: J00228; AAC82527.1; ALT_INIT.
 DR PIR: A02146; GHU.
 DR PDB: 1FC1; 15-JUL-92.
 DR PDB: 1FC2; 15-JUL-92.
 DR MIM: 147100;
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig-cl.
 DR InterPro: IPR003600; Ig-like.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00407; IG1; 2.
 DR SMART: SM00410; IG-like; 1.
 DR PROSITE: PS00290; IG_MHC; 2.
 DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW 3D-structure. 1 1
 FT NON_TER 1 98 CHI.
 FT DOMAIN 1 98 HINGE.
 FT DOMAIN 99 110 CH2.
 FT DOMAIN 111 223 CH2.
 FT DOMAIN 224 330 CH3.
 FT DISULFID 27 83
 FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT CARBOHYD 180 180
 FT MOD_RES 330 330
 FT VARIANT 97 97
 FT VARIANT 239 239
 FT VARIANT 241 241
 FT STRAND 123 126
 FT HELIX 130 134
 N-LINKED (GLCNAC...).
 REMOVED POST-TRANSLATIONALLY.
 K -> R (IN GIM(3) MARKER).
 /FTid-VAR_003886.
 D -> E (IN GIM(NON-1) MARKER).
 /FTid-VAR_003887.
 L -> M (IN GIM(NON-1) MARKER).
 /FTid-VAR_003888.

FT TURN 136 137
 FT STRAND 141 148
 FT STRAND 158 162
 FT TURN 163 164
 FT STRAND 165 166
 FT STRAND 175 178
 FT STRAND 183 190
 FT HELIX 193 197
 FT TURN 198 199
 FT STRAND 202 206
 FT STRAND 215 219
 FT STRAND 227 227
 FT STRAND 230 234
 FT STRAND 238 240
 FT TURN 241 242
 FT STRAND 245 256
 FT STRAND 260 266
 FT TURN 267 268
 FT STRAND 269 270
 FT STRAND 274 276
 FT STRAND 280 281
 FT TURN 283 284
 FT STRAND 287 296
 FT HELIX 297 301
 FT TURN 302 303
 FT STRAND 306 312
 FT TURN 313 314
 FT TURN 316 317
 FT STRAND 320 324
 SQ SEQUENCE 330 AA; 36106 MW; 3770BE106C2FA33D CRC64;
 Query Match 69.9% Score 1758; DB 1: Length 330;
 Best Local Similarity 99.1% Pred. No. 4.4e-115;
 Matches 327; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 141 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200
 DB 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
 QY 201 GLYSLSVVTVPPSSSLGTQYICNVNHNKPSNTKVDKRVKPSCKDTHTCPPCPAPPELLGG 260
 DB 61 GLYSLSVVTVPPSSSLGTQYICNVNHNKPSNTKVDKRVKPSCKDTHTCPPCPAPPELLGG 120
 QY 261 PSVFLFPPKPRDTLMISRTPEVTCVVVDVSHEDPEVFNFYVDGVGVHNAKTKPREQYN 320
 DB 121 PSVFLFPPKPRDTLMISRTPEVTCVVVDVSHEDPEVFNFYVDGVGVHNAKTKPREQYN 180
 QY 321 STYRVSVLTALVDLGVDSYNGVHNGKPKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
 DB 181 STYRVSVLTALVDLGVDSYNGVHNGKPKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
 QY 381 MTRKNOVSLTCLVKGFPYSDIAVESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRW 440
 DB 241 LTRNQVSLTCLVKGFPYSDIAVESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRW 300
 QY 441 QGQNVFSCSVHHEALHNHYTQKSLSLSPGK 470
 DB 301 QGQNVFSCSVHHEALHNHYTQKSLSLSPGK 330
 RESULT 2
 GC2_HUMAN
 ID GC2_HUMAN STANDARD; PRT; 326 AA.
 AC P01859;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE IG GAMMA-2 CHAIN C REGION.
 GN IGHG2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82197621; PubMed=6804948;
 RA Ellison J.W., Hood L.E.;
 RT "Linkage and sequence homology of two human immunoglobulin gamma
 heavy chain constant region genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
 RN [2]
 RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
 RX MEDLINE=81007873; PubMed=6774012;
 RA Wang A.-C., Tung E., Fudenberg H.H.;
 RT "The primary structure of a human IgG2 heavy chain: genetic,
 evolutionary, and functional implications.";
 RL J. Immunol. 125:1048-1054(1980).
 RN [3]
 RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
 RX MEDLINE=80001357; PubMed=113060;
 RA Connell G.E., Parr D.M., Hofmann T.;
 RT "The amino acid sequences of the three heavy chain constant region
 domains of a human IgG2 myeloma protein.";
 RL Can. J. Biochem. 57:758-767(1979).
 RN [4]
 RP SEQUENCE OF 238-275 (ZIE).
 RX MEDLINE=80114419; PubMed=118920;
 RA Hofmann T., Parr D.M.;
 RT "A note of the amino acid sequence of residues 381-391 of human
 immunoglobulins gamma chains.";
 RL Mol. Immunol. 16:923-925(1979).
 RN [5]
 RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 RA Hofmann T., Parr D.M.;
 RL Submitted (MAR-1980) to the PIR data bank.
 RN [6]
 RP SEQUENCE OF 1-121 (DOT).
 RX MEDLINE=95255298; PubMed=7737190;
 RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RT "Characterization of the two unique human anti-flavin monoclonal
 immunoglobulins.";
 RL Eur. J. Biochem. 228:886-893(1995).
 RN [7]
 RP DISULFIDE BONDS.
 RX MEDLINE=72033500; PubMed=4940472;
 RA Milstein C., Frangione B.;
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
 RL Biochem. J. 121:217-225(1971).
 RN [8]
 RP DISULFIDE BONDS.
 RX MEDLINE=69064124; PubMed=5782707;
 RA Frangione B., Milstein C., Pink J.R.L.;
 RT "Structural studies of immunoglobulin G.";
 RL Nature 221:145-148(1969).
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; V00554; CAB58438.1; -
 DR PIR; A02148; G2HU.
 DR MIM; 147110; -
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003600; Ig_Like.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; IgC1; 2.
 DR SMART; SM00410; Ig_Like; 1.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1

FT DOMAIN 1 98 CHI.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 219 CH2.
 FT DOMAIN 220 326 CH3.
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 83
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 140 200
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 FT MOD_RES 326 326
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 FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;
 SQ
 Query Match 64.0%; Score 1610; DB 1; Length 326;
 Best Local Similarity 91.8%; Pred. No. 8e-105;
 Matches 303; Conservative 10; Mismatches 13; Indels 4; Gaps 2;
 QY 141 ASTKGPVFPFLAPSSKSTSGTAAALGCLVKDYPPPTVTVSNWNSGALISGVHTFFAVLQSS 200
 DB 1 ASTKGPVFPFLAPSSKSTSGTAAALGCLVKDYPPPTVTVSNWNSGALISGVHTFFAVLQSS 60
 QY 201 GLYSLSWVTPVSSSLGTQYICNVNHPKSNKVDKRVKPKSCDKTHTCPCPAPPELLGG 260
 DB 61 GLYSLSWVTPVSSSLGTQYICNVNHPKSNKVDKRVKPKSCDKTHTCPCPAPPELLGG 116
 QY 261 PSVFLFPKPKDILMISRTPEVTCVYVDVSHEDPEVKFNMVYDGVGVHNAKTKPREQYN 320
 DB 117 PSVFLFPKPKDILMISRTPEVTCVYVDVSHEDPEVKFNMVYDGVGVHNAKTKPREQYN 176
 QY 321 STVRVSVLVHLDQDLNGKEYCKVSNKALPAPIETKISKAKQPREPQVYITLPPSREE 380
 DB 177 STFRVSVLVHLDQDLNGKEYCKVSNKGLPAPIETKISKAKQPREPQVYITLPPSREE 236
 QY 381 MTKNOVSLTCLVKGFPSPDIWVESNGQPNENYKTPPVLDSDGSEFSLYSLKLVNDSRW 440
 DB 237 MTKNOVSLTCLVKGFPSPDIWVESNGQPNENYKTPPVLDSDGSEFSLYSLKLVNDSRW 296
 QY 441 QQGNVFCVSWHEALHNHYTKSLSPGK 470
 DB 297 QQGNVFCVSWHEALHNHYTKSLSPGK 326
 RESULT 3
 GC4_HUMAN
 ID GC4_HUMAN STANDARD; PRT; 327 AA.
 AC P01861;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 20-AUG-2001 (Rel. 40, Last annotation update)
 DE IG GAMMA-4 CHAIN C REGION.
 GN IGHG4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83157104; PubMed=6299662;
 RA Ellison J.W., Buxbaum J.N., Hood L.E.;
 RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
 RL DNA 1:11-18(1981).
 RN [2]
 RP SEQUENCE OF 1-30 AND 81-326.
 RX MEDLINE=70207560; PubMed=4192699;
 RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
 RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
 constant region of a gamma 4 chain.";
 RT

RL Biochem. J. 117:33-47(1970).
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CC -----
DR EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A02150; G4HU.
DR MIM; 147130; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Igcl; 2.
DR SMART; SM00410; Ig_Like; 1.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DOMAIN 1 98
FT DOMAIN 99 110 CH1.
FT DOMAIN 111 220 HINGE.
FT DOMAIN 221 327 CH2.
FT DOMAIN 328 370 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 141 201
FT DISULFID 247 305
SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;

Query Match 63.6%; Score 1599.5; DB 1; Length 327;
Best Local Similarity 91.8%; Pred. No. 4.3e-104;
Matches 303; Conservative 9; Mismatches 15; Indels 3; Gaps 1;

QY 141 ASTKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPTVTSNNSGALTSGVHTFPAVLQSS 200
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPTVTSNNSGALTSGVHTFPAVLQSS 60
QY 201 GLYSLSSVTVTPSSSLGTQTVICNVNHNKPSNTKVDKVEPKSCDKTHTCCPCPAPELLGG 260
Db 61 GLYSLSSVTVTPSSSLGTQTVICNVNHNKPSNTKVDKVEPKSCDKTHTCCPCPAPELLGG 117
QY 261 PSVFLFPPKPKDTLMISRTPEVTCVVYVDSHEDPEVFNKFNVDGVEVHNKTKPREQYN 320
Db 118 PSVFLFPPKPKDTLMISRTPEVTCVVYVDSHEDPEVFNKFNVDGVEVHNKTKPREQYN 177
QY 321 STYRVSVLVVHLQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 380
Db 178 STYRVSVLVVHLQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 237
QY 381 MTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 440
Db 238 MTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 297
QY 441 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
Db 298 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 327

RESULT 4
GC_RABIT STANDARD; PRT; 323 AA.
AC P01870;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA CHAIN C REGION.
OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
RN NCBI_TaxID=9986;
RP SEQUENCE FROM N.A.
RX MEDLINE=84030930; PubMed=6313520;
RA Bernstein K.E., Alexander C.B., Mage R.G.;
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
RT F-I haplotype."
RL Immunogenetics 18:387-397(1983).
RN [2]
RP SEQUENCE OF 1-128.
RX MEDLINE=76135469; PubMed=1243651;
RA Pratt D.M., Mole L.E.;
RT "Sequence studies on the constant region of the Fd sections of rabbit
RT immunoglobulin G of different allotype."
RL Biochem. J. 151:337-349(1975).
RN [3]
RP SEQUENCE OF 88-266 FROM N.A.
RX MEDLINE=83299917; PubMed=6193512;
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
RL heavy chain and identification of two genomic C gamma genes."
RN Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN [4]
RP SEQUENCE OF 132-161.
RX MEDLINE=70110015; PubMed=5461106;
RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT "Sequence studies of the Fd section of the heavy chain of rabbit
RT immunoglobulin G."
RL Biochem. J. 116:249-259(1970).
RN [5]
RP SEQUENCE OF 129-131 AND 155-322.
RX Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
RL (In) Killander J. (eds.);
RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
RL Stockholm (1967).
CC CC -1- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
CC 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
CC MARKERS AND REF 5 THE E15 MARKER.
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CC -----
DR EMBL; M16426; AAA31289.1; -.
DR PIR; A02161; GHRB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig-cl.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Igcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 N -> E (IN REF. 2).
FT CONFLICT 71 71 V -> VPV (IN REF. 2).
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 173 173 N -> D (IN REF. 5).
FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 Q -> E (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 N -> D (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> D (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE (DISEASE PROTEIN WIS).
 RX MEDLINE=81021548; PubMed=6774747;
 RA Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
 RT "Primary structure of human gamma 3 immunoglobulin deletion mutant:
 RT gamma 3 heavy-chain disease protein Wis.";
 RL Biochemistry 19:4304-4308(1980).
 (2)
 RP REVISIONS TO 12-97 OF PROTEIN WIS.
 RX MEDLINE=77118561; PubMed=402363;
 RA Michaelson T.E., Frangione B., Franklin E.C.;
 RT "Primary structure of the 'hinge' region of human IgG3. Probable
 RT quadruplication of a 15-amino acid residue basic unit.";
 RL J. Biol. Chem. 252:883-889(1977).
 (3)
 RP REVISIONS TO 59-289 OF PROTEIN WIS (DISEASE PROTEIN ZUC).
 RX MEDLINE=77021516; PubMed=823945;
 RA Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
 RT "The amino acid sequence of 'heavy chain disease' protein ZUC.
 RT Structure of the Fc fragment of immunoglobulin G3.";
 RL Biochem. Biophys. Res. Commun. 71:907-914(1976).
 (4)
 RP SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
 RX MEDLINE=82247835; PubMed=6808505;
 RA Alexander A., Steimetz M., Barritault D., Frangione B.,
 RA Franklin E.C., Hood L., Buxbaum J.N.;
 RT "Gamma Heavy chain disease in man: cDNA sequence supports partial
 RT gene deletion model.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
 CC -1- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
 CC INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
 CC NORMALLY PRESENT IN THE HINGE REGION.
 CC -1- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
 CC -1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
 CC REF.2.
 CC -1- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
 CC AND ALL OF THE CHI REGION.
 CC -1- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
 CC OF THE CHI REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
 CC GAMMA-3 HEAVY CHAINS.
 CC -1- MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
 CC OR ANOTHER GAMMA CHAIN SUBCLASS.
 CC -1- MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
 CC TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
 CC IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
 CC SEGMENT (12-28).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; J00231; AAA52805.1; ALT_SEQ.
 DR PIR; A02149; G3HUWI.
 DR MIM; 147120;
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_cl.
 DR InterPro; IPR003600; Ig_like.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00407; IGcl; 1.
 DR SMART; SM00410; IG_like; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 FT DOMAIN 12 73
 FT HINGE.
 FT DOMAIN 74 183
 FT CH2.
 FT DOMAIN 184 289
 FT CH3.

FT REPEAT 29 43
 FT REPEAT 44 58
 FT REPEAT 59 73
 FT MOD_RES 1 1
 FT CARBOHYD 6 6
 FT DISULFID 7 7
 FT DISULFID 24 24
 FT DISULFID 27 27
 FT DISULFID 33 33
 FT DISULFID 39 39
 FT DISULFID 42 42
 FT DISULFID 48 48
 FT DISULFID 54 54
 FT DISULFID 57 57
 FT DISULFID 63 63
 FT DISULFID 69 69
 FT DISULFID 72 72
 FT CARBOHYD 140 140
 FT MOD_RES 290 290
 FT VARIANT 126 127
 FT VARIANT 134 134
 FT VARIANT 139 139
 FT VARIANT 182 182
 FT VARIANT 227 227
 FT VARIANT 227 227
 FT VARIANT 279 279
 SQ SEQUENCE 290 AA; 32331 MW; 569C95705B2F46 CRC64;
 Query Match 46.2%; Score 1162; DB 1; Length 290;
 Best Local Similarity 91.4%; Pred. No. 8.4e-74;
 Matches 212; Conservative 11; Mismatches 9; Indels 0; Gaps 0;
 QY 239 EPKSCDTHTCPCPAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 298
 DB 59 EPKSCDTPPCPCPAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 118
 QY 299 NWYVDGVEVHNKTKPREOVNSTRVYVSVLTVLHQDLNGKEYKCKVSNKALPAPIEKT 358
 DB 119 KWIYDGVQVHNKTKPREQVFNSTRVYVSVLTVLHQDLNGKEYKCKVSNKALPAPIEKT 178
 QY 359 ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGYFSPDAVWEESNGQPENNYKTPP 418
 DB 179 ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGYFSPDAVWEESNGQPENNYKTPP 238
 QY 419 PVLDSGSEFFLYSKLTVDKSRWQQGNFSCSVMHEALHNHYTQKSLSLSPGK 470
 DB 239 PMLDSGSEFFLYSKLTVDKSRWQQGNFSCSVMHEALHNHYTQKSLSLSPGK 290
 RESULT 7
 GC1_RAT
 ID GC1_RAT STANDARD; PRT; 326 AA.
 AC P20759;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG GAMMA-1 CHAIN C REGION.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89232738; PubMed=3149946;
 RA Brueggemann M.;

"Evolution of the rat immunoglobulin gamma heavy-chain gene family.";

RT Gene 74:473-482(1989).
 RL PIR: PS0017; PS0017.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_c1.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00407; IGcl; 2.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 FT NON_TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 112 HINGE.
 FT DOMAIN 113 219 CH2.
 FT DOMAIN 220 326 CH3.
 FT DISULFID 27 82
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 140 200
 FT DISULFID 246 304
 FT CARBOHYD 176 176
 SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;.

Query Match 45.9%; Score 1155; DB 1; Length 326;
 Best Local Similarity 63.4%; Pred. No. 3e-73;
 Matches 211; Conservative 52; Mismatches 60; Indels 10; Gaps 4;

QY 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
 DB 1 AETAPSVYPLAPGTALSKSMVTLGCLVKGYFPEPVTVSWNSGALTSGVHTFPAVLQ-S 59
 QY 201 GLYSSVVYVPSSSLGITQYICNVNHPKSTKVDKRVKPEKSCDKTHCTPCPAPELLGG 260
 DB 60 GLYLTSSVYVPSSTWPSQVTCNVNHPASSTKVDKRVKPEKSCDKTHCTPCPAPELLGG 113
 QY 261 ---PSVFLFPKPKDILMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQY 317
 DB 114 SEVSVFIFPPKPKDILMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQY 173
 QY 318 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPS 377
 DB 174 QFNSTFRSVELPILHODWLNKGRFRCKPTSAAPFSPKTEKTSKRGTPQVPHVYTMSP 233
 QY 378 REEMTKNOVSLTCLVKGYFPEPSDIKAVESNGQPENNYKTTTPVLDSDGSEFELYSLKLTVDK 437
 DB 234 KEEMTQNEVSVTCWKYGYFPDIIYVQWQNGQPENNYKTTTPVLDSDGSEFELYSLKLTVDK 493
 QY 438 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
 DB 294 EKWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 326

RESULT 8
 GC3_MOUSE STANDARD; PRT; 329 AA.
 AC P22436;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE IG GAMMA-3 CHAIN C REGION, SECRETED FORM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85027161; PubMed=5092053;
 RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
 RA Tucker P.W., Blatner F.R.;
 RT "Structural analysis of the murine IgG3 constant region gene."
 RL EMBO J. 3:2041-2046(1984).

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 CC -----
 CC EMBL; J00451; -; NOT_ANNOTATED_CDS.
 DR PIR: B02156; G3M5C.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR003600; Ig_like.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00407; IGcl; 2.
 DR SMART: SM00410; IG_like; 1.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Transmembrane; Alternative splicing.
 FT NON_TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 113 HINGE.
 FT DOMAIN 114 223 CH2.
 FT DOMAIN 224 327 CH3.
 SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 45.7%; Score 1150; DB 1; Length 329;
 Best Local Similarity 65.0%; Pred. No. 6.7e-73;
 Matches 215; Conservative 44; Mismatches 68; Indels 4; Gaps 3;

QY 142 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 201
 DB 1 TTTAPSVYPLVPGSDTSGSSVTLGCLVKGYFPEPVTVSWNSGALTSGVHTFPAVLQ-SG 59
 QY 202 LYSLSVVYVPSSSLGITQYICNVNHPKSTKVDKRVKPEKSCDKTHCTPCPAPELLG 259
 DB 60 FVLSLTVVPSSTWPSQVTCNVNHPASSTKVDKRVKPEKSCDKTHCTPCPAPELLG 118
 QY 260 GPSVFLFPKPKDILMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQY 319
 DB 119 GPSVFLFPKPKDILMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQY 178
 QY 320 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSRE 379
 DB 179 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSRE 238
 QY 380 EMTKNQVSLTCLVKGYFPEPSDIKAVESNGQPENNYKTTTPVLDSDGSEFELYSLKLTVDKSR 439
 DB 239 QMSKKVSLTCLVTNFFSEALSVWERNGELEDQYKNTPTPILDSGTYFLYSLKLTVDTS 298
 QY 440 WQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
 DB 299 WQGNVFCSCVMHEALHNHYTQKSLSLSPGK 329

RESULT 9
 GC1_MOUSE STANDARD; PRT; 324 AA.
 ID AC P01868;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE IG GAMMA-1 CHAIN C REGION.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80045036; PubMed=115593;
 RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,

RA Takahashi N., Mano Y.;
 RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
 RL gamma 1 chain gene.";
 RL Cell 18:559-568(1979).
 [2]
 RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
 RX MEDLINE=80202559; PubMed=6769752;
 RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
 Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
 RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
 RT cloned in a bacterial plasmid.";
 RL Gene 9:87-97(1980).
 [3]
 RN SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
 RP MEDLINE=80012837; PubMed=113776;
 RX Rogers J., Clarke P., Salsner W.;
 RA "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
 RT heavy chain.";
 RT Nucleic Acids Res. 6:3305-3321(1979).
 [4]
 RN SEQUENCE (MYELOMA PROTEIN MOPC 21).
 RP MEDLINE=78242288; PubMed=98524;
 RX Adetugbo K.;
 RA "Evolution of immunoglobulin subclasses. Primary structure of a
 RT murine myeloma gamma 1 chain.";
 RL J. Biol. Chem. 253:6068-6075(1978).
 [5]
 RN DISULFIDE BONDS (MOPC 21).
 RP MEDLINE=73008889; PubMed=5073237;
 RX Svasti J., Milstein C.;
 RA "The disulphide bridges of a mouse immunoglobulin G1 protein.";
 RL Biochem. J. 126:837-850(1972).
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 CC -----
 DR EMBL; V00793; CAA24172.1; -;
 DR EMBL; V00793; CAA24173.1; -;
 DR EMBL; V00793; CAA24174.1; -;
 DR EMBL; V00793; CAA24175.1; -;
 DR EMBL; V00795; CAA24176.1; -;
 DR PIR; A02159; GLMS.
 DR GlycoSuiteDB; P01868; -;
 DR MGD; MGI:96446; Igh-4.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_c1.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; Igcl; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Alternative splicing.
 FT NON_TER 1
 FT DOMAIN 1
 FT DOMAIN 98
 FT DOMAIN 111
 FT DOMAIN 218
 FT DISULFID 27
 FT DISULFID 102
 FT DISULFID 104
 FT DISULFID 107
 FT DISULFID 109
 FT DISULFID 138
 FT CARBOHYD 174
 FT CH1.
 FT HINGE.
 FT CH2.
 FT CH3.
 FT INTERCHAIN (WITH A LIGHT CHAIN).
 FT INTERCHAIN (WITH A HEAVY CHAIN).
 FT INTERCHAIN (WITH A HEAVY CHAIN).
 FT INTERCHAIN (WITH A HEAVY CHAIN).
 FT N-LINKED (GLCNAC. . .).
 FT /FTid=CAR_000055.
 FT DISULFID 244
 FT MOD_RES 324
 FT CONFLICT 276
 FT CONFLICT 278

SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;
 Query Match 45.5%; Score 1145; DB 1; Length 324;
 Best Local Similarity 62.3%; Pred. No. 1.5e-72;
 Matches 207; Conservative 55; Mismatches 60; Indels 10; Gaps 4;
 QY 141 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVWNSGALTSGVHTFPAVLQSS 200
 DB 1 AKTTTPSVYPLAPGAAQTNSMTLGLCLVKGYFPEPTVTWNSGSLSSGVHTFPAVLQSD 60
 QY 201 GLYSLSSVYVTPSSSLGTQTYICNVNHNKPSNTKVKRRPEKSCDKTHTCPP--CPAPELL 258
 DB 61 -LYTLSSSVYVTPSSPRSETVTCNVAHPASSTKVKIVPRDCG---CKPCICVPEV- 114
 QY 259 GGPSVFLPPPKDYLMIKSRTPETVTCVVVDVSHEDPEVKFNYVDGVEVHNKATKPRERQ 318
 DB 115 --SSVFIEFPKPKDVLITLTPKVTCTVVVDISKDDPEVQFSWFVDDVEVHTAQTQPRERQ 172
 QY 319 YNSTYRVSVLTVLHODWLNKGKCYKSNKALPAIEKTIKAKGQPREPOVYITLPPSR 378
 DB 173 FNSTRSVSELPIMHQDWLNGKEFKCRVNSAFAFPAPIETISIKTRKRPAPQVYITPPPK 232
 QY 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFSLYSLKLTVDKS 438
 DB 233 EQMAKDQVSLTCMITDFPEDITVEQWNGQPAENYKNTQPIMTNTNGSVFVYSLKLVQKS 292
 QY 439 RWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
 DB 293 NWEAGNTFTCSVLHRELHNHHTKSLSHSPGK 324
 RESULT 10
 GCB_RAT ID GCB_RAT STANDARD; PRT; 333 AA.
 AC P20761;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG GAMMA-2B CHAIN C REGION.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89232738; PubMed=3149946;
 RA Brueggemann M.;
 RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
 RL Gene 74:473-482(1988).
 DR PIR; PS0018; PS0018.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_c1.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; Igcl; 2.
 DR SMART; SM00410; IG_Like; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1
 FT DISULFID 15
 FT DISULFID 15
 FT DISULFID 27
 FT DISULFID 80
 FT DISULFID 106
 FT DISULFID 109
 FT DISULFID 112
 FT DISULFID 115
 FT DISULFID 147
 FT DISULFID 253
 FT DISULFID 311
 FT INTERCHAIN (WITH A LIGHT CHAIN).
 FT INTERCHAIN (WITH A HEAVY CHAIN).
 FT INTERCHAIN (WITH A HEAVY CHAIN).
 FT INTERCHAIN (WITH A HEAVY CHAIN).
 FT INTERCHAIN (WITH A HEAVY CHAIN).
 FT INTERCHAIN (WITH A HEAVY CHAIN).
 SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;
 Query Match 45.5%; Score 1144.5; DB 1; Length 333;
 Best Local Similarity 63.7%; Pred. No. 1.6e-72;


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CC -----
DR EMBL; V00798; CAA24178.1; -.
DR PIR; A02152; G2MSA.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IgC1; 2.
DR SMART; SM00410; Ig_MHC; 1.
DR PROSITE; PS00290; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;

Query Match 44.9%; Score 1129; DB 1; Length 330;
Best Local Similarity 63.9%; Pred. No. 1.9e-71;
Matches 212; Conservative 43; Mismatches 73; Indels 4; Gaps 3;

QY 141 ASTKGPSVFPPLAPSSKSTSGTAALGCLVKDYPEPVTVSWNSGALTSVGHVTFPAVLQSS 200
DQ 1 AKTAPSVYPLAPVCGDTTSSVTLGCLVKGYPEPVTLVNWSGSLSSGVHTFPVLQSD 60

QY 201 GLYSLSSVTVVPSSSLGTQYICNVNHPKNTKVDKRVKPCDKTKHTCPP--CPAPELL 258
DQ 61 -LVTLSSTVTVSTSSQSTICVNAHPASSTKVDKIEPRG-PTIKPCPPCKCAPNLL 118

QY 259 GGSVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREQ 318
DQ 119 GGSVFLFPKPKDKDMLISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREQ 178

QY 319 YNSTYRVSVTLVHODWLNKGYKCKVSNKALPAPIETKISKAKGQPREPVYTLPPSR 378
DQ 179 YNSTLRVVSALPQHQDWMGSKGKCKVNNKDLPAPIETKISKAKGQPREPVYTLPPPE 238

QY 379 EEMTKNOVSITCLVKGYPSDIAVWESNGOPENNYKTPPVLDSGDSFFLYSKLTVDKS 438
DQ 239 EEMTKNOVSITCLVKGYPSDIAVWESNGOPENNYKTPPVLDSGDSFFLYSKLTVDKS 298

QY 439 RWQGNVFSVSVHVALHNYTKSLSPGK 470
DQ 299 NWVERNSYSCSVVHEGLHNHHTTKSFRTPGK 330

RESULT 14
GCC_RAT STANDARD; PRT; 329 AA.
AC P20762;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA-2C CHAIN C REGION.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN NCBI_TaxID=10116;
RP SEQUENCE FROM N.A.
RX MEDLINE=88166903; PubMed=3127222;
RA Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
region cDNA: extensive homology to mouse gamma 3.";
RL Eur. J. Immunol. 18:317-319(1988).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X07189; CAA30169.1; -.
DR PIR; S00847; S00847.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IgC1; 2.
DR SMART; SM00410; Ig_LIKE; 1.
DR PROSITE; PS00290; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 222 CH2.
FT DOMAIN 223 329 CH3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 143 203
FT DISULFID 249 307
SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;

Query Match 44.8%; Score 1127.5; DB 1; Length 329;
Best Local Similarity 62.8%; Pred. No. 2.4e-71;
Matches 209; Conservative 51; Mismatches 66; Indels 7; Gaps 3;

QY 141 ASTKGPSVFPPLAPSSKSTSGTAALGCLVKDYPEPVTVSWNSGALTSVGHVTFPAVLQSS 200
DQ 1 ARTAPSVYPLVPGCSGTSGTLGCLVKGYPEPVTVKNWSGALSSGVHTFPVLQ-S 59

QY 201 GLYSLSSVTVVPSSSLGTQYICNVNHPKNTKVDKRVKPCDKTKHTCPP--CPAPEL 257
DQ 60 GLYSLSSVTVVPSSVQVTCVAHPATKSNLIKRIEPR--RPRPRPTDICSDDN 116

QY 258 LGGSVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREE 317
DQ 117 LGPSVFIFFPKPKDILMITLTPKVTCTVVDVSEEDVQFQSFVFNVRVFTAQTPHEE 176

QY 318 QYNSTYRVSVTLVHODWLNKGYKCKVSNKALPAPIETKISKAKGQPREPVYTLPPS 377
DQ 177 QLNGTFRVSTLHQDWMGSKGKCKVNNKDLPSPIETKISKPRGKARTPQVYTIPTP 236

QY 378 REEMTKNOVSITCLVKGYPSDIAVWESNGOPENNYKTPPVLDSGDSFFLYSKLTVDK 437
DQ 237 REEMTKNOVSITCLVKGYPSDIAVWESNGOPENNYKTPPVLDSGDSFFLYSKLTVDK 296

QY 438 SRWQGNVFSVSVHVALHNYTKSLSPGK 470
DQ 297 DSNMRGDIYTCVVHVALHNNHHTKNSLSPGK 329

RESULT 15
GCC_MOUSE STANDARD; PRT; 335 AA.
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA-2A CHAIN C REGION, B ALLELE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 24, 2002, 15:13:10 ; Search time 86.76 Seconds
(without alignments)
792.393 Million cell updates/sec

Title: US-09-499-662-89
Perfect score: 2515
Sequence: 1 MGWSCIIILFVATATGVHSQ.....MHEALHNNHYTKSLSPCK 470

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTEMBL_17.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1628.5	64.8	473	11 Q9D8L4	Q9D8L4 mus musculus
2	1617.5	64.3	463	11 Q99LC4	Q99LC4 mus musculus
3	1577.5	62.7	473	11 Q99L25	Q99L25 mus musculus
4	1551	61.7	468	11 Q99L31	Q99L31 mus musculus
5	1440.5	57.3	437	11 Q99L44	Q99L44 mus musculus
6	846	33.6	500	4 Q9BRV0	Q9BRV0 homo sapien
7	751.5	29.9	597	4 Q9BU10	Q9BU10 homo sapien
8	751	29.9	484	11 Q99LA6	Q99LA6 mus musculus
9	747.5	29.7	597	4 Q9BQB8	Q9BQB8 homo sapien
10	728.5	29.0	487	11 Q99KA4	Q99KA4 mus musculus
11	653	26.0	479	11 Q99M22	Q99M22 mus musculus
12	602	23.9	426	11 Q9DCD9	Q9DCD9 mus musculus
13	569.5	22.6	416	4 Q9NPP6	Q9NPP6 homo sapien
14	509	20.2	150	4 Q9Y298	Q9Y298 homo sapien
15	492	19.6	137	4 Q95978	Q95978 homo sapien
16	480.5	19.1	384	4 Q9UP60	Q9UP60 homo sapien
17	458	18.2	119	4 Q9UL94	Q9UL94 homo sapien
18	454	18.1	117	11 Q9QXF0	Q9QXF0 mus musculus
19	452.5	18.0	124	4 Q9UL92	Q9UL92 homo sapien

20	446	17.7	119	5 Q9GYZ2	Q9GYZ2 schistosoma
21	444	17.7	125	4 Q9UL95	Q9UL95 homo sapien
22	438	17.4	117	11 Q9QXE9	Q9QXE9 mus musculus
23	433.5	17.2	118	11 Q9Z1C4	Q9Z1C4 mus musculus
24	432.5	17.2	116	4 Q9UL89	Q9UL89 homo sapien
25	429.5	17.1	114	11 Q9JL81	Q9JL81 mus musculus
26	428.5	17.0	147	4 Q9Y509	Q9Y509 homo sapien
27	425.5	16.9	110	11 Q9JL77	Q9JL77 mus musculus
28	409	16.3	111	11 Q9D9B8	Q9D9B8 mus musculus
29	407.5	16.2	109	11 Q9JL75	Q9JL75 mus musculus
30	399	15.9	117	11 Q9Z1C6	Q9Z1C6 mus musculus
31	399	15.9	375	4 Q9BSZ1	Q9BSZ1 homo sapien
32	396	15.7	684	13 Q90544	Q90544 ginglymosto
33	377.5	15.0	110	11 Q9JL83	Q9JL83 mus musculus
34	363.5	14.5	298	11 Q9QYF0	Q9QYF0 mus musculus
35	359	14.3	120	4 Q9BUA1	Q9BUA1 homo sapien
36	348	13.8	109	11 Q9JL85	Q9JL85 mus musculus
37	325	12.9	113	4 Q9UL90	Q9UL90 homo sapien
38	316	12.6	121	4 Q9UL71	Q9UL71 homo sapien
39	315.5	12.5	118	4 Q9UL91	Q9UL91 homo sapien
40	315	12.5	131	4 Q9UL88	Q9UL88 homo sapien
41	312.5	12.4	112	4 Q9HCC1	Q9HCC1 homo sapien
42	307.5	12.2	122	4 Q9UL84	Q9UL84 homo sapien
43	306	12.2	116	4 Q9UL93	Q9UL93 homo sapien
44	298.5	11.9	118	4 Q9UL72	Q9UL72 homo sapien
45	294.5	11.7	150	4 Q95973	Q95973 homo sapien

ALIGNMENTS

RESULT 1
Q9D8L4
ID Q9D8L4 PRELIMINARY; PRT; 473 AA.
AC Q9D8L4;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE 1810060009RIK PROTEIN.
GN 1810060009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP
RC SEQUENCE FROM N.A.
RC SPRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuoka H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochava H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikolaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staehli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Rono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S.,
RA Hayashizaki Y.;
Functional annotation of a full-length mouse cDNA collection.;
Nature 409:685-690(2001).
-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
EMBL: AK007918; BAE25349.1; -;
MGD: MGI:1924014; 1810060009RIK.
DR InterPro; IPR003599; Ig.

InterPro: IPR003597; Ig-cl.
 DR InterPro: IPR003600; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig_4.
 DR SMART: SM00409; Ig_2.
 DR SMART: SM00407; IGL1; 3.
 DR SMART: SM00406; IGV; 1.
 DR SMART: SM00410; IG_Like; 1.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
 DR SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 64.8%; Score 1628.5; DB 11; Length 473;
 Best Local Similarity 63.4%; Pred. No. 1.7e-125;
 Matches 302; Conservative 70; Mismatches 95; Indels 9; Gaps 4;

QY 1 MGWSCIIFLVATATGVHSQVQLVQSGAEVKKPGASVKVYKSCASGYTFTSYNMQWVKQAP 60
 DB 1 MEWIVFLFSLTGTAGVHSQVQLVQSGAEVKKPGASVKVYKSCASGYTFTSYNMQWVKQAP 60
 QY 61 GORLEWNGEIDPSDSTYNNQKFKGKATLVDTVSASTAYMELSSLSRSEDATVYYCARNRD 120
 DB 61 GORLEWNGEIDPSDSTYNNQKFKGKATLVDTVSASTAYMELSSLSRSEDATVYYCARNRD 120
 QY 121 YSNWTFDVGEGTITVSSASTKGPSVFLPAPSSKTSSTGGTAAALGCLVKDYFPEPTVTS 180
 DB 121 YSYD-LFAYWGQGLTVTSAAKTTPSPVYPLAFGSAQAOTNSMVTGLGKVGYPEPEVTYT 179
 QY 181 WNSGALTSGVHTTTPAVLQSSGLYSLSVTVTPSSSLGTGTIYICNVNHNKPSNTKVKRVEP 238
 DB 180 WNSGSLSSGVHTTTPAVLQSD-LYTLSSSVTVPSSTPSETVTCNVAHVPASSTKVDKKIYP 238
 QY 241 KSCDTHHTCTPP--CPAPELIGGSPVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKF 298
 DB 239 RDCG-----CKPCICTVPEV---SSVFIFPPKPKDVLITLTTPKVTCTVVDISKDDPEVQF 291
 QY 299 NWTVDGVFVHNAKTKPREQYNSTYRVVSVLTVLHODWLNKGRYKCKVSNKALPADIET 358
 DB 292 SMFVDVVEVHTAQTPREEQFNSTFRSVSELPIMHODWLNKGRYKCKVSNKALPADIET 351
 QY 359 ISKAKGQPREPOVYITLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 418
 DB 352 ISKTRKRPKAPQYITLPPKPEQNAKDKVSLTCTMTITDFPEDITVEWMQNGQPAENKNTQ 411
 QY 419 PVLDSGSEFSLYSLTKLVDRSRQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 470
 DB 412 PIMDTGSGFYIYKLVNQQSNKEAGNTFTCSVLHLEGLHNHTKEKLSLHSPGK 463

RESULT 3
 Q99L25 PRELIMINARY; PRT; 473 AA.
 ID Q99L25
 AC Q99L25;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC003888; AAH03888.1; -.
 SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 62.7%; Score 1577.5; DB 11; Length 473;
 Best Local Similarity 63.2%; Pred. No. 2.6e-121;
 Matches 300; Conservative 61; Mismatches 107; Indels 7; Gaps

QY 1 MGWSCIIFLVATATGVHSQVQLVQSGAEVKKPGASVKVYKSCASGYTFTSYNMQWVKQAP 60
 DB 1 MEWSWVFLFSLTGTAGVHSQVQLVQSGAEVKKPGASVKISCKVSGYTFDTHTIHWVKQP 60
 QY 61 GORLEWNGEIDPSDSTYNNQKFKGKATLVDTVSASTAYMELSSLSRSEDATVYYCARNRD 120
 DB 61 EGGLEWIGIYPRDGTSTKYNEKFKGKATLTADKSSSTAYMQNLSTSEDSAVYCFCSRGS 120
 QY 121 --YSNN-WYFDVWEGTTLTVSSASTKGPSVFLPAPSSKTSSTGGTAAALGCLVKDYFPEPV 177
 DB 121 IYGYGLYFDYWGQGTITVSSAKTAPSVYPLAPVCDGTTGSSVTLGCLVKGYFPEPV 180
 QY 178 TVSNWNGALTSGVHTTTPAVLQSSGLYSLSVTVTPSSSLGTGTIYICNVNHNKPSNTKVKDR 237
 DB 181 TLTWNSGSLSSGVHTTTPAVLQSD-LYTLSSSVTVTPSSVTSQITCNVAHPASSTKVDKVK 239

Query Match 64.3%; Score 1617.5; DB 11; Length 463;
Best Local Similarity 63.3%; Pred. No. 1.3e-124;
Matches 299; Conservative 72; Mismatches 90; Indels 11; Gaps 5;

```
QY 238 VEPKSCDKTHCTPP--CPAPELGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPE 295
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 240 IEPRG-PTIKPCPPCKAPNLLGGPSVFIFPKIKDVLMSLSPMVTCVVVDSEDDPD 298

QY 296 VKFNWYDGVGVHNAKTPREQYNSTYRVVSVLTVLHQDLNKGKEYCKVSKNKPAPI 355
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 299 VQISFVNNVEVLTQTHREDYNSLTVVSAIPQIQHDMGSGKEFKCKVNNKALPAPI 358
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 356 EKTSKAKGPREPQVYTLPPSREEMTKNOVSLTCLVKGYFSPDIAVEWESNGOPENNYK 415
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 359 ERTSKPKGSRAPQVTVLPPPEEMTKKOVITLCMTWDFMEDYVFWTNNKTELNLYK 418
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 416 TTPPVLDSDGSFFLYSKLTVDKRWQGNVFCSCVMHEALHNHYTKLSLSPCK 470
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 419 NTEPVLDSDGSYFMYSKLREKKNWVERNSYSCSVVHEGLNHHHTTKFSRTPK 473

RESULT 4
Q99L31 PRELIMINARY; PRT; 468 AA.
AC Q99L31;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AA03878.1; -
SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match 61.7%; Score 1551; DB 11; Length 468;
Best Local Similarity 62.5%; Pred. No. 3.8e-119;
Matches 295; Conservative 62; Mismatches 109; Indels 6; Gaps 4;

QY 1 MWSCILFLVATGATGHSQVLVQSGAEYKPKGASVKVCKASGYFTTSYWMQWVKQAP 60
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MKCSWVIFFLMAVIGVNSEVLOQSGAELVRPGASVKLSCTASGFNIKDSLHWHVQRP 60
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 61 GQLEWNGEIDPDSYNTYKQKPKATLVDTASATYMWELSLRSEDATVYICARNRD 120
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 EQLEWIGWIDPEGETKYPKFDKATITADTSSNTAYLQLSLSTSEDATVYICARNLL 120
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 121 YSNWYFDVWEGEGLTVTSASTKGPSVFLPAPSSKSTSGTAAAGCLVLDVDPPEVTVS 180
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 YGG--YDYWGQGTITVSSAKTAPSVYPLAPVCGDTTGSSTVTLGCLVKGYPEPVLT 178
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 181 WNSGALTSVGHVTPAVLQSGLSYLSVWTVPPSSLTQTYICNVNHPKNTKVKRKEVP 240
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 179 WNSGSLSSGVHTPEVAVLQSD-LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEP 237
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 241 KSCDKTHCTPP--CPAPELGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKF 298
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 238 RG-PTKPCPPCKAPNLLGGPSVFIFPKIKDVLMSLSPMVTCVVVDSEDDPDVQI 296
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 299 NWYDGVGVHNAKTPREQYNSTYRVVSVLTVLHQDLNKGKEYCKVSKNKPAPIEKT 358
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 297 SWFVNNVEVLTQTHREDYNSLTVVSAIPQIQHDMGSGKEFKCKVNNKALPAPIERT 356
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 359 ISKAKGPREPQVYTLPPSREEMTKNOVSLTCLVKGYFSPDIAVEWESNGOPENNYKTP 418
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 357 ISKPKGSRAPQVTVLPPPEEMTKKOVITLCMTWDFMEDYVFWTNNKTELNKYKTE 416
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 419 PVLDSDGSFFLYSKLTVDKRWQGNVFCSCVMHEALHNHYTKLSLSPCK 470
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 417 PVLDSDGSYFMYSKLREKKNWVERNSYSCSVVHEGLNHHHTTKFSRTPK 468
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```
RESULT 5
Q9RIA4 PRELIMINARY; PRT; 437 AA.
AC Q9RIA4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE GAMMA1 HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G.; Yu X.; Ekramoddoullah A.K.M.; Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF152372; AA040243.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match 57.3%; Score 1440.5; DB 11; Length 437;
Best Local Similarity 59.3%; Pred. No. 4.1e-110;
Matches 268; Conservative 72; Mismatches 95; Indels 17; Gaps 7;

QY 21 VQLVQSGAEYKPKGASVKVCKASGYFTTSYWMQWVKQAPQGRLEWNGEIDPDSYNTYN 80
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 VQLQESGGGLVKPGSLKLSCAASGFTFSYAMSWVRQTPKEKLEWVASEF-SGGIIVYT 59
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 81 QKEKGAATLVDTASATYMWELSLRSEDATVYICARNRDYSNWYFDVWEGEGLTVTVSS 140
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60 DSVKGRFTIYKDKDRNLTSLQMSLSRSEDATVYICARG-DYS-----AYWGPGLVTVSA 113
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 141 ASTKGPSVFLPAPSSKSTSGTAAAGCLVLDVDPPEVTVSNWNSGALTSVGHVTPAVLQSS 200
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 114 AKTTPPSVYPLAPGSAQTNSMTVTLGCLVKGYPEPVTVTNWNSGSLSSGVHTPPAVLQSD 173
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 201 GLYSLSVWTVPPSSLTQTYICNVNHPKNTKVKDKVEPKSCDKTHCTPP--CPABELL 258
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 174 -LYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKVDKKIVPRDCG----CKPICITVPEV- 227
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 259 GGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQ 318
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 228 --SSVFLFPKPKDVLITLTPKVTCTVVVDLSDKDDPEVQFSWFVDDVEVHTAQTPREEQ 285
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 319 YNSTYRVSVLTVLHQDLNKGKEYCKVSKNKPAPIEKTISKAKGPREPQVYTLPPSP 378
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 286 FNSTFRSVSELPIMHQDLNKGKEYCKRVNSAAPAPIEKTISKTRKPAQVYTIIPPK 345
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 379 EEMTKNOVSLTCLVKGYFSPDIAVEWESNGOPENNYKTPPVLDSDGSFFLYSKLTVDKS 438
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 346 EQMAKDKVSLTCTMTDFPEDITVWQWNGQPAENYKTPQIMDTDGSYFYSLNVAQKS 405
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 439 RWQGNVFCSCVMHEALHNHYTKLSLSPCK 470
   :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 406 NWEAGNTFTCSVLHGLNHHHTTKNLSHPCK 437
```

```
RESULT 6
Q9BRV0
ID Q9BRV0 PRELIMINARY; PRT; 500 AA.
AC Q9BRV0:
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:14588).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005951; AA005951.1; -.
SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

Query Match 33.68; Score 846; DB 4; Length 500;
Best Local Similarity 40.78; Pred. No. 3e-61;
Matches 204; Conservative 66; Mismatches 179; Indels 50; Gaps 18;

Qy 1 MGWSCIIILFVATATGVSQVQVQSGAEVKKPGASVKVSKASGYTFTSYMMQWVKQAP 60
Db 1 MDWTMSILFLVAATGAQSQVHLVQSGAEVMSPGASRVSKTSGYAFHTYSIIIVRQAP 60
Qy 61 GQLEWGEIDPSDSTNYNOKFKGKATLVDTASTAYMELSLRSEDATVYYCARNR- 119
Db 61 GQLEWGEIDPSDSTNYNOKFKGKATLVDTASTAYMELSLRSEDATVYYCARNR- 119
Qy 61 GQLEWGEIDPSDSTNYNOKFKGKATLVDTASTAYMELSLRSEDATVYYCARNR- 119
Db 61 GQLEWGEIDPSDSTNYNOKFKGKATLVDTASTAYMELSLRSEDATVYYCARNR- 119
Qy 120 DYS---NNWYF---DVGCEGLTVVSSASTKGPSVFPLAPSSKSTSGGTALGLVLDYF 173
Db 120 DYS---NNWYF---DVGCEGLTVVSSASTKGPSVFPLAPSSKSTSGGTALGLVLDYF 173
Qy 121 SYSSQNDYIIYYMDVMGKGTITVSSASPTSPKVFPLSLCS--TOPDGNVVIACLVQGF 179
Db 121 SYSSQNDYIIYYMDVMGKGTITVSSASPTSPKVFPLSLCS--TOPDGNVVIACLVQGF 179
Qy 174 P-EPVTVSNWNGALTSVHTPPAVLQSGG-LYSLSSVTVTPSSS-LGTQTVICNVNPKS 230
Db 180 PQEPLSVTWSESGGVITARNPPQDASGDLTYTSSQLTLPATOCLAGKSVTCHVKHY-T 238
Qy 231 NTKVDKRVPEKSCDKTHCPCPAPPELLGGPSVFLFPPKPK-----DTLM 275
Db 239 NPSQDVTY-----PCPVSPPTPTSPST-PPTSPSCCHPRLSLHRLPALEDDL 285
Qy 276 ISRTPETCVVVDVSHEDPEVKFNWYDGVGVHNAKTPREQYNSTYRVSVLTVLHQD 335
Db 286 LGSEANLTCTLTGL-RDASGVTFFTWTPSSGK--SAVGGPPDRDLCCGYSVSSVLSCAEP 342
Qy 336 WLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPVYTLPPSREMTKNQ-VSLTCLVKG 394
Db 343 WNHGKTTCTAAYPEKSTPLTATLSKS-GNTRFEVHLPPPSSEALNELVITCLARG 401
Qy 395 FYPDSIAVWESNQ--PENNYKTPPVLD--SDG--SFFLYSKLTVDKSRQGNVFS 449
Db 402 FSPKDLVLRWLGQSQELPREKYLWASRQEPSQGTTFITFAVTSILRVAEDKKGDTFSCM 461
Qy 450 VMHEALHNHYTKLSLSPCK 470
Db 462 VGHEALPLAFTQETIDRLAGK 482

RESULT 7
Q9BU10
ID Q9BU10 PRELIMINARY; PRT; 597 AA.
AC Q9BU10:
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:1652).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
SEQUENCE FROM N.A.
TISSUE-LYMPHOMA;
Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
EMBL; BC002963; AA002963.1; -.
SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;

Query Match 29.98; Score 751.5; DB 4; Length 597;
Best Local Similarity 31.28; Pred. No. 2.1e-53;
Matches 180; Conservative 91; Mismatches 188; Indels 117; Gaps 17;

Qy 8 LFLVATATGVSQVQVQSGAEVKKPGASVKVSKASGYTFTSYMMQWVKQAPGORLEWM 67
Db 8 LLLVAAPRWVLSQVLOQWAGLLKPSSETLSLTCGVYSGFSGYWWSIROPKGLSEMI 67
Qy 68 GEIDPDSSTNYNOKFKGKATLVDTASTAYMELSLRSEDATVYYCAR-----NRDYS 122
Db 68 GEINSGS--TNYNPSLSKRSVTISVDTSKQLSLKSSVNAADTAVYYCARVITRASPGTD 126
Qy 123 NNWYFDVWGEGLTVVSSASTKGPSVFPLAPSSKSTSG--GTAALGCLVKDYFPEPVTVSW 181
Db 127 GRYGMDVMGQGTITVTVSSGSASAPTLFPLVSCENSPSDTSSVAVGCLAQDLPSDITFSW 186
Qy 182 --NSGALTSGVHTTTPAVLOSGLYSLSVTVTPSSSL--GTQTY--ICNVNPKPSN----- 231
Db 187 KYKNSDISSTRGPFPSVLR--GGKYAATSQVLLPSKQVMDQGTDEHVWCKVQHPNGNKEKV 245
Qy 232 -----TKVDKRVPEKPS-----CDKTHTCP----- 250
Db 246 PLPVIAELPPKVSFVFPDRGFFGNPKRSKLICATGFSRQIQVSWLRQCKQVSGVYT 305
Qy 251 -PCPAPELLGGPS----- 262
Db 306 DQVQAEAKESGPTTYKYVTSTLTIKESDWLSQSMFTCRVDHRLGLTFQONASSMVCVPDQDTA 365
Qy 263 --VFLEPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTPREQYN 320
Db 366 IRVFAIPPS--FASIFLTKSKTLCLVTLDTLTYD--SVTISWTRQNGEAVKTHNTISEHPN 423
Qy 321 STYRWVSVTLVHODWLNGLKREYCKVSNKALPAPIEKTIKAKGQ--REPOVYTLPPSRE 379
Db 424 ATFSAVGEASICEDDWSNGERFTCTVHTDLPSPKLTISRPKGVALLHRPDIYLLPPARE 483
Qy 380 EMT--KNQVSLTCLVKGFYPSDIAVWESNGQ--ENNYKTPPVLD--SDGSFFLYSKLT 434
Db 484 QLNRESATITCLTGTGFSPADVFQVMQGRQLSPKYSPEKYVTSAPMPQAPGRYFAHSILT 543
Qy 435 VDKSRWQGNVFSQVSMHEALHNHYTKLSLSPCK 470
Db 544 VSEEWNTGETYTCVVAHEALPNRVTERTVDKSTGK 579

RESULT 8
Q99LA6
ID Q99LA6 PRELIMINARY; PRT; 484 AA.
AC Q99LA6:
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:6319).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HAMMARY TUMOR;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
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DR EMBL; BC003495.1; -.
SQ SEQUENCE 484 AA; 52567 MW; 8EAE4F9BCF582FA CRC64;

Query Match 29.9%; Score 751; DB 11; Length 484;
Best Local Similarity 36.5%; Pred. No. 1.8e-53;
Matches 176; Conservative 89; Mismatches 189; Indels 28; Gaps 16;
Qy 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPKGASVKVSKASGYTFTSYMMQWVKQAP 60
Db 1 MAWWTLLFLAAGSIQAQIQVQSGPELKKPGFTVSKASGYTFTSYMMHVKQAP 60
Qy 61 GORLEWGEIDPSDSTYNNQKFKGKATLTVDTSASTAYMELSSLRSEDATVYYCARNRD 120
Db 61 CKGLKMWGWNIEGTESVYADDFKGRFAFSLTASSTIHLQINNKLKEDTATYFCARS-D 119
Qy 121 YSNMNY-FDVRCGTLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKKDYFPE-PVT 178
Db 120 YDYLIIAMDYWGQGTSTVTVSSSARNPTIYPLT-LPPALSSDPVITIGCLIHDFPSGTMN 178
Qy 179 VSNWNGALTVGHVTPFAVLQSSGLYSLSSVTVTPSSSLGT-QTYICNVNHNKPSNTKVDKR 237
Db 179 VTWCKSGKDIITVNEPPALASGRYTMSSQLTLPAVECPGESVKCSVQH-DSNPVQELD 237
Qy 238 VEPKCDKTHCTPCPCAPPELLGGPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVK 297
Db 238 V---NCSGPTPPPTITPSC--QPSLSLQRPALD-LLLGSDASITCTLNGLRNPEGAV- 290
Qy 298 FNWYVDGVEVHNATKPREEQYNST--YRVVSVLTVLHODWLNKKEYCKVSKNKAAP 354
Db 291 FTW-----EPSTGDAVKKAVQNSCGYSSVSLPGLCAERWNSGASFCTVTHPE-SGT 344
Qy 355 IEKTSKAKGPREPQVYTLPPSREEMTKNQ-VSLTCLVKGYPSPDIAVENESNQ--P 410
Db 345 LTGIIAKVTVNTFPPQVHLLPPPSSEALNELLSTLCVRAFNKEVLRWLHGNELSP 404
Qy 411 ENNYKTPPVLDSG--SFFLYSKLTVDKSRWQGNVFCSCVMHEALNHNHYTKLSLSLP 468
Db 405 ESYLVFELKPEPGEGATTYLVTSVLRVSAETWKGQDOYSCMVGHGHEALPMNFTQKTIDRLS 464
Qy 469 GK 470
Db 465 GK 466

RESULT 9
Q9BQB8 PRELIMINARY; PRT; 597 AA.
AC Q9BQB8;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:1905) (PROTEIN FOR MGC:1228).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=RIADOMYOSARCOMA;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPHOMA;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006180.1; -.
DR EMBL; BC001872.1; AAH01872.1; -.
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 29.7%; Score 747.5; DB 4; Length 597;

Best Local Similarity 31.1%; Pred. No. 4.5e-53;
Matches 179; Conservative 91; Mismatches 189; Indels 117; Gaps 17;
Qy 8 LELVATATGVHSQVQLVQSGAEVKKPKGASVKVSKASGYTFTSYMMQWVKQAPGORLEWM 67
Db 8 LLLVAAPRWLVLSQVQLQOQAGALLKPKSETLSLTCGVYGSFSGYYSWIKOPKGLLEWI 67
Qy 68 GEIDPSDSTYNNQKFKGKATLTVDTSASTAYMELSSLRSEDATVYYCAR-----NRDYS 122
Db 68 GEINHS-GITNYPNPSLKSRTVISVDTSKKQLSLKSSVNAADATVYYCARVITRASPGTD 126
Qy 123 NNWYEDVWGEGLTVTVSSASTKGPSVFPPLAPSSKSTSG-GTAALGCLVKKDYFPEPVTWS 181
Db 127 GRYGMVWGQGTSTVTVSSGSASAPTLFPLVSCENSPDTSSTSSVAVGCLAQDFLPSDITSF 186
Qy 182 --NSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSL--GTQTY-ICNVNHNKPSN----- 231
Db 187 KYKNNSDISSTRGFPFSLR-GGKYAATSQVLLPSKDVMOGTDEHVCKVQHPNGNKEKNV 245
Qy 232 -----TKYDKRVEPKS-----CDKTHTCP----- 250
Db 246 PLPVIAELPPKVSFVFPVPRDGFPGNPKSKLICQATGFSRQIQVSWLRGKQVSGVTT 305
Qy 251 -PCPAPELLGGPS----- 262
Db 306 DQVQAEAKESGPTTKVTSTLTIKESDWSQSMTFCRVDRHGLTFOQNASSMCMVPPQDQA 365
Qy 263 --VELFPPPKDMLISRTPEVTCVVVDVSHEDPEVKENWYDGVVHNKAKTPREBOYN 320
Db 366 IRVFAIPPS-FASIFUTKSTKLTLVDLDTYD-SVTISWTRONGEAVKTHTWISHPN 423
Qy 321 STYRVSVLTVLHODWLNKKEYCKVSKNKAAPIEKTSKAKGQP-REPQVYTLPPSRE 379
Db 424 ATFSAVGEASICEDDWNSSGERFCTVTHDLPSPKQATISRPKGVALHRPDVLLPPARE 483
Qy 380 EMT-KNQVSLTCLVKGYPSPDIAVENESGQP--ENNYKTPPVLVD--SDGSFFLYSKLT 434
Db 484 QLNRESATITCLVTGFSPADYFVQWQGRQGLSPKEKYVTSAPMPPEQAPGRYFAHSILT 543
Qy 435 VDKSRWQGNVFCSCVMHEALNHNHYTKLSLSLSPGK 470
Db 544 VSEEWNTGETYTCVVVAHEALPNRVTERIVDKSTGK 579

RESULT 10
Q99KA4 PRELIMINARY; PRT; 487 AA.
AC Q99KA4;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:6727).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004786.1; AAH04786.1; -.
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96D333077B CRC64;

Query Match 29.0%; Score 728.5; DB 11; Length 487;
Best Local Similarity 35.1%; Pred. No. 1.3e-51;
Matches 170; Conservative 89; Mismatches 196; Indels 29; Gaps 15;
Qy 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPKGASVKVSKASGYTFTSYMMQWVKQAP 60
Db 1 MNFGSLIFLVLVLKGVQCEQLVSGGLVPGGSLKLSAASGFTFSYAMSWVRQTP 60
Qy 61 GORLEWGEIDPSDSTYNNQKFKGKATLTVDTSASTAYMELSSLRSEDATVYYCARN-- 118

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Db 61 ERLEWATISDGGSYTYYPDMVKGRTISRDNKNNLYLQMSLKSEDTAMYCARDMG 120
Qy 119 -RDYSNNYFDYWGEGTLVTSSASTKGPSVPLAPSSKSTGGTAALGLVKDYEPPE-P 176
Db 121 GSPYGGYSRFDYWGOGTTITVSSSARNPTIYPLT-LPRALSSDDPVIICGLIHDYFPST 179
Qy 177 VTVSNMGALTSQVHTFPAVLQSSGLYSLSSVTVTPSSSLGT-QTYICNVNHPKSNKTV 235
Db 180 MNVTGKSGKDTTNNFPALASGGYTMSSQLTLPAVECPGESVKCSVQH---DSNAV 236
Qy 236 KRVEPKSODKTHUTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPE 295
Db 237 QELDVKCSGPPPCPCP-PSG--HPSLSLQRPALD-LLGSDASLTCTLGNLRNPEGA 292
Qy 296 VKFNNYVDGVEVHNAKTPREQYNST---YRVSVLTVLHODWLNKGYCKVSKNALP 352
Db 293 V-FTW-----EPSTGKDAVQKAVONSCGYSVSVLPGCAERNWSGASFCKTCTVTHPESD 346
Qy 353 APIEKTISKAKQPREQVYTLPPSREEMTKNQ-VSLTCLVKGFVPSDIAVEWESNGQ-- 409
Db 347 T-LTGCTIAKITVNTFPPQVHLLPPSEELALNELSLTCLVRAFNPKEVLVRLHGNEL 405
Qy 410 -PENNYKTPPVLDSDG--SFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSL 466
Db 406 SPESYLVEPLKEPGEGATYLVTSVLRVSAETWKQDQYSCWVGHEALPMNFTQKTIDR 465
Qy 467 SPKG 470
Db 466 LSGK 469
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RESULT 11
Q99M22
ID Q99M22 PRELIMINARY; PRT; 479 AA.
AC Q99M22;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR MCG:6342).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-MAMMARY TUMOR;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002091; AA02091.1.;
SQ SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;

Query Match 26.0%; Score 653; DB 11; Length 479;
Best Local Similarity 33.8%; Pred. No. 1.9e-45;
Matches 161; Conservative 90; Mismatches 193; Indels 32; Gaps 18;

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Qy 7 ILFLVATATGSHSQVLQVSGAEVKKPGASVKVSCKASQSTFTS-YVMQWVKQAPQRL 65
Db 6 LYLTLATPGILSDVQLQSGGLVKPQSLSLTSVTSYTSYGYWNWIRQFPGNKLE 65
Qy 66 WMGEIDPSDSTYNQKFKGATLVDTASATYAMELSSRLSEDTAVYICARNRDYSNNW 125
Db 66 WMGYIN-YDGSNNYNPGLKNSRISITRDTSKNOFFLKLNSVTEDTATYCA-SRGYS-- 120
Qy 126 YFDVWNGEGLTVTSASATKGPSVFLAPSSKSTGGTAALGLVKDYEPPE-PVTVSWNSG 184
Db 121 WFPNMNGTGLTVTSASARNPTIYPLT-LPPALSSDDPVIICGLIHDYFPSTGMNVTGKS 179
Qy 185 ALTSQVHTFPAVLQSSGLYSLSSVTVTPSSSLGT-QTYICNVNHPKSNKTVDKRVEPKS 243
Db 180 GKDITVNFPPALASGGRYTMSSQLTLPAVECPGESVKCSVQH-DSNPVQELDV---NC 235
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Qy 244 DKHTHTCCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYD 303
Db 236 SGPPTPPPTIPSC--QPSLSLQRPALD-LLGSDASITCTLGNLRNPEGAV-FTW--- 288
Qy 304 GVEVHNAKTPREQYNST---YRVSVLTVLHODWLNKGYCKVSKNALPAPIEKTIS 360
Db 289 --EPSTGKDAVQKAVONSCGYSVSVLPGCAERNWSGASFCKTCTVTHPE-SGTLTG 345
Qy 361 KAKGQPREQVYTLPPSREEMTKNQ-VSLTCLVKGFVPSDIAVEWESNGQ---PENNYKT 416
Db 346 KVTVNTFPPQVHLLPPSEELALNELSLTCLVRAFNPKEVLVRLHGNELSPESYL 405
Qy 417 TTPVLDSDG--SFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 470
Db 406 EPLKEPGEGATYLVTSVLRVSAETWKQDQYSCWVGHEALPMNFTQKTIDRLSGK 461
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RESULT 12
Q9DCD9
ID Q9DCD9 PRELIMINARY; PRT; 426 AA.
AC Q9DCD9;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE ADULT MALE KIDNEY CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE CLONE:0610041A01, FULL INSERT SEQUENCE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AK002875; BAB22422.1; -;
DR InterPro; IPR003599; Ig_-;
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00410; IG-like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 426 AA; 45819 MW; 56E1275BA48F6FB1 CRC64;

Query Match 23.9%; Score 602; DB 11; Length 426;
Best Local Similarity 32.6%; Pred. No. 2.5e-41;
Matches 157; Conservative 75; Mismatches 165; Indels 84; Gaps 16;

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Qy 1 MGWSCIILFLVATATGHSQVQLVQSGAEVKKPGASVKYSCKASGYTFTSYWQWVKQAP 60
Db 1 MGFSRIFLFLSVSYG----- 16
Qy 61 GQRLWMEIDPDSYTYNOKFKGKATLTVDTSASTAYMELSSLSRSEDATVYYCARNRD 120
Db 17 -----NGDTSYNOKFKGKATLTVDKSSSTAYMOLSSLTSDSAVYFCARS-D 62
Qy 121 YSNWNWYFDVWGEGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE-PVTY 179
Db 63 YYGPYAMDYWGQGTSTVTSSESARNPTIYPLT-LPRALLSSDPVIIGCLIHDFSPGTWNV 121
Qy 180 SWNSGALTSQVHTFPVAVLQSSGLYSLSVTVTPSSSLGT-QTYICNVNHHKPSNTKVDKRV 238
Db 122 TWGSGKIDITVNFPPALAGGGTMSQSLTPAVECEGESVKCSVOH---DSNAVOEL 178
Qy 239 EPKSCDRTHTCPPCAPPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKF 298
Db 179 DVKCSGPPPCPCP-PSC--HPSLSLQRPALD-LLLGSDASLTCTLGLRNPGEAV-F 233
Qy 299 NWYVDGVEVHNATKPREEQNST---YRVVSVLTVLHQDWLNGKEYCKKYSNKPALPAPI 355
Db 234 TW-----EPSTGKDAVQKAVQNSCGCYSVSSVLPGCAERNWNSGASFKCTVTHPESDT-L 287
Qy 356 EKTISKAKGQPREPOVYTLPPSREMTKNO-VSLTCLVKGFYPSDIAVWESNGQ---PE 411
Db 288 TGTIAKTIVNTFPQVHLLPPSEELALNELVSLTCLVRAFPKPEVLVRLHNGEELSPE 347
Qy 412 NNYKTTTPVLDSDG--SFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 469
Db 348 SYLVEFLKPEGEGATTLVTSVLRVSAELWKQDQGYSCMVGHEALPMNFTQKTDRLSG 407
Qy 470 K 470
Db 408 K 408

RESULT 13
Q9NPP6 PRELIMINARY; PRT; 416 AA.
AC Q9NPP6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE IMMUNOGLOBULIN HEAVY CHAIN VARIANT (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Pluvinet R., Estivill X., Escarceller M., Sumoy L.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RT "The European IMAGE consortium for integrated molecular analysis of
human gene transcripts."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
DR EMBL; AL389978; CAB97534.1; -.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR SMART; SM00410; IG_Like; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
FT NON_TER 1
SQ SEQUENCE 416 AA; 44786 MW; 8C41708BB8AB4687 CRC64;
```

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Query Match 22.6%; Score 569.5; DB 4; Length 416;
Best Local Similarity 35.0%; Pred. No. 1.1e-38;
Matches 148; Conservative 66; Mismatches 172; Indels 37; Gaps 17;

Qy 60 PQORLEWMEIDPDSYTYNOKFKGKATLTVDTSASTAYMELSSLSRSEDATVYYCARNR 119
Db 1 PKGLEWYSRISSSGDVTDIADSVKGRFTVSRDTAKNSLSLQMSLSLRVEDTAVYYCAR-- 58
Qy 120 DYSNNWY-FDVWGEGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE-PV 177
Db 59 ----TYYGMDWVGQGTTVTVSSASPTSPKVPFLSLDS-TPQDGNVVVACLVQGFPPQEP 113
Qy 178 TVSNWNGALTSQVHTFPVAVLQSSG-LYSLSSVTVTPSSSL-GTQTYICNVNH--KPSNTK 233
Db 114 SVTWSESGQNTARNFPSPQDASGLYTTSSQLTLPATQCPDGKSVTCHVKHYTNPSQ-- 171
Qy 234 VDKRVEPKSCDTHTCPPCAPPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVVDVSHED 293
Db 172 -----DVTVPFVPPPPPC-HPRLSLHRALED-LLLGSEANLTCTLTGL-RDA 218
Qy 294 PEVKENWYVDGVEVHNATKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKKYSNKPALPA 353
Db 219 SGATFTWTPSSGK--SAVQGPPEPDLGGCYSVSSVLPGCAQPNWGHGETTCTAAHPELKT 276
Qy 354 PIEKTISKAKGQPREPOVYTLPPSREMTKNO-VSLTCLVKGFYPSDIAVWESNGQ--P 410
Db 277 PLTANITKS-GWTFPEVHLLPPSEELALNELVTLTCLARGSPKDVLRVLMQSGQELP 335
Qy 411 ENNYKTTTPVLD-SDG--SFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLS 467
Db 336 REKYLTVASRQPSQGTTFFAVTSILRVAAEDKKGDTFCMVVGHEALPLAFTQKTDIDL 395
Qy 468 PKG 470
Db 396 AGK 398

RESULT 14
Q9Y298 PRELIMINARY; PRT; 150 AA.
ID Q9Y298
AC Q9Y298;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE IGG VH PROTEIN PRECURSOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RA MEDLINE-98322155; PubMed-9657749;
RT Jacquemin M.G., Vander Elst L.P.L.;
RT "Mechanism and kinetics of factor VIII inactivation: study with an
IgG4 monoclonal antibody derived from a hemophilia A patient with
inhibitor."
RL Blood 92:496-506(1998).
CC -|- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
DR EMBL; AJ224083; CAAL1829.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR SIGNAL 1
FT NON_TER 150
SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;
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Query Match 20.2%; Score 509; DB 4; Length 150;

Best Local Similarity 66.2%; Pred. No. 2.8e-34;
Matches 100; Conservative 15; Mismatches 32; Indels 4; Gaps 1;

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QY 1 MCWSCIIILFLVATATGVHSQVQLVSGAEVKKPGASVKVSCKASGYTFTSYHWQVVKQAP 60
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MDWTRWFLVAAATGTHAQVQLVSGAEVKKPGASVKVSCKASGYTFTSYHWQVVKQAP 60
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 GORLEWMMGEIDPDSYTNYNOKFKGKATLVDTSTASTAYMELSSLRSEDYAVYICARNRD 120
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 GGLWVGSGFDPESESIYAREFQGSVTWTDSTDIAYMELSSLRSDDTAVYICA---- 116
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 YSNWYFDVWGEGLTVTVSSASTKGPSVPEPL 151
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 117 VPDPAFDIWGQGTMTVTVSSASTKGPSVPEPL 147
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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RESULT 15
O95978
ID O95978 PRELIMINARY; PRT; 157 AA.
AC O95978;
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE VH1 PROTEIN PRECURSOR (FRAGMENT).
GN VH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PERIPHERAL BLOOD;
RA Jox A., Zander T., Kueppers R., Irsch J., Kanzler H., Kornacker M.,
RA Bohlen H., Diehl V., Wolf J.;
RT "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a
RT patient with mixed cellularity Hodgkin's disease is associated with
RT somatic mutations within the untranslated regions of rearranged and
RT class switch recombinated Ig genes.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AJ005570; CAA06599.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Signal.
FT SIGNAL 1 21 POTENTIAL.
FT NON_TER 157 157
SQ SEQUENCE 157 AA; 17304 MW; 86986EDDA84D88B5 CRC64;
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Query Match 19.6%; Score 492; DB 4; Length 157;
Best Local Similarity 61.1%; Pred. No. 7.5e-33;
Matches 96; Conservative 20; Mismatches 41; Indels 0; Gaps 0;

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QY 1 MCWSCIIILFLVATATGVHSQVQLVSGAEVKKPGASVKVSCKASGYTFTSYHWQVVKQAP 60
   | : | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MDWTRVFLVAVPGVHSQVQLVSGAEIKRPGASVKVHCKTSGYFTSYIHWVROPR 60
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 GORLEWMMGEIDPDSYTNYNOKFKGKATLVDTSTASTAYMELSSLRSEDYAVYICARNRD 120
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 GGLWMMGGIGPGVGSWCAEKFGQLTMTNTSTTVYMELSLRFEEDYAVYFCGRGR 120
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 YSNWYFDVWGEGLTVTVSSASTKGPSVPEPLAPSKS 157
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 WRSGNYNGHWGGTPTVTVSSSTKGPSVPEPLAPCSRS 157
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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